

24995

From: Hamud, Fozia  
Sent: Wednesday, January 22, 2003 3:59 PM  
To: STIC-Biotech/ChemLib  
Subject: sequence search for 09/714,792

Please, search SEQ ID NO: 4 of 09/714, 792 against commercial and interference data bases. Thanks.

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308-8891

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Point of Contact  
P. Sheppard  
Telephone number: (703) 308-4499

Searcher: \_\_\_\_\_  
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Location: \_\_\_\_\_  
Date Picked Up: \_\_\_\_\_  
Date Completed: 1/29/03  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:  
NA Sequences: \_\_\_\_\_  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 24, 2003, 19:33:59 ; Search time 14 Seconds

(without alignments)  
1125.786 Million cell updates/sec

Title: US-09-714-792a-4

Perfect score: 2104  
Sequence: 1 MAFVCLAICGLYFLISTTF.....LLLRKPNTYPKMIPEFCDT 380

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

rchd: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2104	100.0	380	1132_HUMAN	014627 homo sapien
2	310.5	14.8	420	1 IL5R_HUMAN	001344 homo sapien
3	298	14.2	424	1 IL31_MOUSE	009030 mus musculu
4	295.5	14.0	427	1 IL31_HUMAN	P78552 homo sapien
5	263	12.5	831	1 PRLR_CHICK	004594 gallus gall
6	247	11.7	415	1 IL5R_MOUSE	P21183 mus musculu
7	238	11.3	831	1 PRLR_MELO	Q91094 meleagris g
8	220	10.5	369	1 CYRG_HUMAN	P31785 homo sapien
9	216.5	10.3	830	1 PRLR_COLLI	090374 columba liv
10	212.5	10.1	369	1 CYRG_MOUSE	P34902 mus musculu
11	208	9.9	373	1 CYRG_CANFA	P40321 canis fami
12	195	9.3	878	1 IL3B_MOUSE	P26954 mus musculu
13	189.5	9.0	379	1 CYRG_BOVIN	Q95118 bos taurus
14	178.5	8.5	897	1 CYRB_HUMAN	P32927 homo sapien
15	173.5	8.2	896	1 CYRB_MOUSE	P26955 mus musculu
16	165	7.8	581	1 PRLR_BOVIN	028172 bos taurus
17	165	7.8	610	1 PRLR_RAT	P05710 rattus norv
18	159	7.6	581	1 PRLR_SHEEP	Q46561 ovis aries
19	159	7.6	608	1 PRLR_MOUSE	Q08501 mus musculu
20	151	7.2	622	1 PRLR_HUMAN	P16471 homo sapien
21	151	7.2	862	1 IL12S_HUMAN	Q96655 homo sapien
22	150.5	7.2	917	1 IL6B_MOUSE	Q00560 mus musculu
23	150	7.1	581	1 PRLR_CEREL	Q28825 cervus elap
24	149	7.1	616	1 PRLR_RABIT	P14787 oryctolagus
25	142.5	6.8	400	1 GPCR_HUMAN	P15509 homo sapien
26	138	6.6	378	1 IL3R_HUMAN	P26951 homo sapien
27	134.5	6.4	1097	1 LIFR_HUMAN	P42702 homo sapien
28	131.5	6.2	630	1 PRLR_ORENI	Q91513 oreochromis
29	128	6.1	874	1 IL12S_MOUSE	P97378 mus musculu
30	126.5	6.0	918	1 IL6B_HUMAN	P40189 homo sapien
31	120.5	5.7	836	1 GCSR_HUMAN	Q90062 homo sapien
32	116.5	5.5	1282	1 DOME_DROME	Q9vw60 drosophila
33	113.5	5.4	1165	1 LEPR_HUMAN	P48357 homo sapien

34	112.5	5.3	1631	1 PTPI_DROME	P35992 drosophila
35	109.5	5.2	918	1 IL6B_RAT	P40190 rattus norv
36	107.5	5.1	638	1 GHR_HUMAN	P10912 homo sapien
37	107.5	5.1	837	1 GCSR_MOUSE	P40223 mus musculu
38	107	5.1	107	1 GHR_BOVIN	P79108 bos taurus
39	106	5.0	634	1 GHR_SHEEP	Q28575 ovis aries
40	105	5.0	511	1 VGLG_VSVO	P04884 vesicular s
41	104.5	5.0	1092	1 LIFR_MOUSE	P42703 mus musculu
42	102.5	4.9	638	1 GHR_PIG	P19786 sus scrofa
43	101.5	4.8	638	1 GHR_RABIT	P19941 oryctolagus
44	99.5	4.7	1162	1 LEPR_RAT	Q62959 rattus norv
45	99	4.7	507	1 EPOR_MOUSE	P14753 mus musculu

## ALIGNMENTS

RESULT 1  
ID 1132\_HUMAN STANDARD: PRT; 380 AA.  
AC 014627; 000667;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Interleukin-13 receptor alpha-2 chain precursor (Interleukin-13 binding protein).  
GN IL13RA2 OR IL13R.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX TISSUE=Renal cell carcinoma;  
RC MEDLINE=96279273; PubMed=8663118;  
RA Caput D., Laurent P., Kaghad M., Lelias J.M., Lefort S., Vita N., Ferrara P.;  
RT "Cloning and characterization of a specific interleukin (IL)-13 binding protein structurally related to the IL-5 receptor alpha chain."  
RT J. Biol. Chem. 271:16921-16926(1996).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX TISSUE=Testis;  
RC MEDLINE=97321053; PubMed=9177784;  
RA Guo J., Apio F., Mellerin M.P., Lebeau B., Jacques Y., Minvielle S.;  
RT "Chromosome mapping and expression of the human interleukin-13 receptor."  
RT Genomics 42:141-145(1997).  
CC - FUNCTION: BINDS AS A MONOMER WITH HIGH AFFINITY TO INTERLEUKIN-13 (IL-13). BUT NOT TO IL-4.  
CC - SUBCELLULAR LOCATION: Type I membrane protein.  
CC - SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.  
CC - SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  
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CC EMBL: X95302; CA64617.1;  
CC EMBL: U70981; AAB17170.1;  
CC EMBL: Y08768; CAA70021.1;  
CC Genew, HGNC:5975; IL13RA2.

DR	MIM:	300130;	-.
DR	InterPro:	IPR002996;	CRIA.
DR	InterPro:	IPR003961;	FN.III.
DR	InterPro:	IPR003532;	Hemtopoptn_S.F2.
DR	Pfam:	PF00041;	fms; 1.
DR	PROSITE:	PS01356;	HEMATOPO_REC-S_F2; 1.
KW	Receptor:	Transmembrane;	Glycoprotein; Signal.
FT	CHAIN	1	26
FT	SIGNAL	1	26
FT	CHAIN	27	380
FT	DOMAIN	27	343
FT	TRANSMEM	344	363
FT	DOMAIN	364	380
FT	DISULFID	145	155
FT	DISULFID	184	197
FT	CARBOHYD	115	115
FT	CARBOHYD	215	215
FT	CARBOHYD	290	290
FT	CARBOHYD	299	299
SO	SEQUENCE	380 AA;	44176 MW; 36CAGIBS56ZCR87 CRC64;

Query Match	100.0%;	Score 2104;	DB 1;	Length 380;
Percent Local Similarity	100.0%;	Pred. NO. 7.8e-166;		
Matches 380;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	MAFQALIGCLYTLTISTTFCGCTSSSDTEIKVNPPODEIYDDPGYLGLXLOMOPPLSLD	60
Db	1	MAFQALIGCLYTLTISTTFCGCTSSSDTEIKVNPPODEIYDDPGYLGLXLOMOPPLSLD	60
QY	61	HEKCEVEYELKYNIGSETWKTITITKLNLYKDDGDLNKGIEAKIHTLLPWOCTNSGEVQ	120
Db	61	HEKCEVEYELKYNIGSETWKTITITKLNLYKDDGDLNKGIEAKIHTLLPWOCTNSGEVQ	120
QY	121	SSAETHYTWISPOSIPEPTKQVDMQCVYYNNQYLLCSMKPGIGVLDDITNYNLFYIEGLDH	180
C3	121	SSAETHYTWISPOSIPEPTKQVDMQCVYYNNQYLLCSMKPGIGVLDDITNYNLFYIEGLDH	180
QY	181	ALQCVDIKADGQNIIGCRFPLEASDYPKDFYICVNGSSENKPIRSSYFTFOLQNIYKPLP	240
Db	181	ALQCVDIKADGQNIIGCRFPLEASDYPKDFYICVNGSSENKPIRSSYFTFOLQNIYKPLP	240
QY	241	PVYLTFTRRESSCEIKLWMSIPLPGIPARCFDEYIEIREDPTLTATAVENETYTLKTTNE	300
Db	241	PVYLTFTRRESSCEIKLWMSIPLPGIPARCFDEYIEIREDPTLTATAVENETYTLKTTNE	300
QY	301	TROLCFVVRKSVNVIYCSDDGIGMSWMSKQCKEGEDLSKTLILRWLPDPGFLILIVITVG	360
Db	301	TROLCFVVRKSVNVIYCSDDGIGMSWMSKQCKEGEDLSKTLILRWLPDPGFLILIVITVG	360
QY	361	LLLRKPNYTPKMIPEFCDDT 380	
Db	361	LLLRKPNYTPKMIPEFCDDT 380	

RESULT 2			
IL5R HUMAN	STANDARD:	PROT:	420 AA.
ID	IL5R HUMAN		
AC	001344;		
DT	01-JUL-1993 (rel. 26, Created)		
DT	01-JUL-1993 (rel. 26, Last sequence update)		
DT	10-OCT-2001 (rel. 40, Last annotation update)		
DE	Interleukin-5 receptor alpha chain precursor (IL-5-alpha) (CD123 antigen).		
GN	IL5RA OR IL5R.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=92372031; PubMed=1505961;		
RA	Scott H.S., Guo X.H., Hopwood J.U., Morris C.P.;		
RT	Structure and sequence of the human alpha-L-iduronidase gene. "		
LT	Genomics 13:1311-1313(1992).		

[2] SEQUENCE FROM N.A.  
RX MEDLINE=9235767; PubMed=1495999;  
RA Tavernier J., Tuypens T., Plaetlinck G., Verhee A., Fiers W.,  
RT "Molecular basis of the membrane-anchored and two soluble isoforms of  
RL the human interleukin 5 receptor alpha subunit."  
RN Proc. Natl. Acad. Sci. U.S.A. 89:7041-7045(1992).

[3]  
RP SEQUENCE OF 1-335 FROM N.A. (S1 FORM).  
RX MEDLINE=92005669; PubMed=1833065;  
RA Tavernier J., Devos R., Cornells S., Tuypens T., van der Heyden J.,  
RT Fiers W., Plaetlinck G.;  
RN "A human high affinity interleukin-5 receptor (IL5R) is composed of  
RT an il5-specific alpha chain and a beta chain shared with the receptor  
for GM-CSF".  
RL Cell 66:1175-1184(1991).

CC - FUNCTION: THIS IS THE RECEPTOR FOR INTERLEUKIN-5. THE ALPHA CHAIN  
CC BINDS TO IL-5.  
CC - SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BETA  
CC CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.  
CC - SUBCELLULAR LOCATION: Type I membrane protein.  
CC - ALTERNATIVE PRODUCTS: 3 ISOFORMS; MEMBRANE-BOUND FORM (SHOWN  
CC HERE), SOLUBLE FORM S1 AND SOLUBLE FORM S2; ARE PRODUCED BY  
CC ALTERNATIVE SPLICING.  
CC - TISSUE SPECIFICITY: EXPRESSED ON EOSINOPHILS AND BASOPHILS.  
CC - SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  
CC - SIMILARITY: TO IL-13 RECEPTOR ALPHA-2 CHAIN.  
CC - DATABASE: NAME=PROV; NOTE=CD guide CDw125 entry;  
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cdw125.htm".

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DR EMBL; M96652; AAA59152.1; -  
DR EMBL; M96651; AAA59151.1; -  
DR EMBL; M75914; AAA36110.1; -  
DR EMBL; A26249; CAA01793.1; -  
DR EMBL; A24587; CAA01731.1; -  
DR EMBL; A26251; CAA01794.1; -  
DR PIR; A40267; A40267.  
DR Genew; HGNC:6017; IL5RA.  
DR MIM; 147851; -  
DR InterPro; IPRO02996; CR1A.  
DR InterPro; IPRO03532; HemtopoLn\_S.F2.  
DR PROSITE; PS01356; HEMATOPOLN\_RC\_SF\_1.  
KW Receptor; Transmembrane; Glycoprotein; Alternative splicing; Signal.

KW SIGNAL 1 20  
FT CHAIN 21 420 INTERLEUKIN-5 RECEPTOR ALPHA CHAIN.  
FT DOMAIN 21 342 EXTRACELLULAR (POTENTIAL).  
FT TRANSSEM 343 362 POTENTIAL.  
FT DOMAIN 363 420 CYTOPLASMIC (POTENTIAL).  
FT CARBOHYD 35 35 N-LINKED (GLCNAC. . . ) (POTENTIAL).  
FT CARBOHYD 131 131 N-LINKED (GLCNAC. . . ) (POTENTIAL).  
FT CARBOHYD 216 216 N-DINKED (GLCNAC. . . ) (POTENTIAL).  
FT CARBOHYD 244 244 N-DINKED (GLCNAC. . . ) (POTENTIAL).  
FT VARSPLOC 333 335 NDE -> FSR (IN SOLUBLE ISOFORM S1).  
FT VARSPLOC 336 420 MISSING (IN SOLUBLE ISOFORM S1).  
FT VARSPLOC 333 333 N -> K (IN SOLUBLE ISOFORM S2).  
FT VARSPLOC 334 420 MISSING (IN SOLUBLE ISOFORM S2).  
SQ SEQUENCE 420 AA; 47700 MW; 420681BFC6B51700 CRC64;

	Query Match	14.8%	Score 310.5;	DB 1;	Length 420;
	Best Local Similarity	26.6%;	Pred. No. 3.2e-18;		
	Matches	99;	Conservative 156;	Indels 47;	Gaps 16;
OY	27 DTEKVNPPDFEVDPEYLGVLVQLQWQPPLSLDHFKECTVEYEELKNINIGSETWKTIIT	86			
	:   :   :   :	:	:	:	:

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Db 25 DEKISLLPVPNETIKVTG-LAQVLLQMKRNPQDEQ-RVNLEPYVKINAKREDDETERT 82
OY 87 KRLHYKDGFDLNGKIEAKIHTLLPMQCTNGSEVSSMAFTTWISPOGIPETKVODMOCV 146
Db 83 ES---KCVTIILKGFSAKYRTILO--NDHSLASSMAAEIHL-APGSGPSTISVNLCTGT 135
OY 147 -----YYNMOYLL-CSWKPGIGVLLDTNLYLFY----WYEGDLHALOCVDYIKAD 191
Db 136 TWTFEDNYSRLKSYQVLSLHCTWLVTGDAPEQYFLFYKYSMTF-----ECQETSKOT 189
OY 192 -GONIGCRFP--YLEASDYKDFYICVNGSSEKPIRSSYTFPOLQNYKPLDPVYLFETR 248
Db 190 LGRNACWCPFPFTILSKGDMLSVLVNGSSKSHAIKPEQDLFALHAIDQINPLWTAETI 249
OY 249 ESSCEIKLKWSPILGPICARCDYEIEIRREDDTLVTANVEEYTKTNTROLCPFY 308
Db 250 EGT-RLSTOWEKPVSAFPHCFDEYKIKHTNRYGLQIEKLTNAFTSIIDLSKRYDVQV 308
OY 309 RSKVNIYCSDDGIMSEWSDKQCEGEDLSKTLRLFWLFPFGILL-----VIFVTGLL 362
Db 309 RAAVSSMCREAGLWSEMS-QPIYGNDEKRP--LREW-----FVIYIMATICPLILLSLI 361
OY 363 LRKPNTYPRMIP 374
Db 362 KCICHLMIKLPF 373

RESULT 3
1131_MOUSE STANDARD: PRT; 424 AA.
AC 009030;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-13 receptor alpha-1 chain precursor (IL-13R-alpha-1) (IL-13RA-1) (interleukin-13 binding protein) (NR4).
GN IL13RA1 OR IL13RA OR IL13R.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP MEDLINE=96133964; PubMed=8552669;
RA Hilton D.J., Zhang J.-G., Metcalf D., Alexander W.S., Nicola N.A.,
RA Willson T.A.;
"Cloning and characterization of a binding subunit of the interleukin 13 receptor that is also a component of the interleukin 4 receptor.";
Proc. Natl. Acad. Sci. U.S.A. 93:497-501(1996).
CC -1- FUNCTION: BINDS IL-13 WITH A LOW AFFINITY. TOGETHER WITH IL-4R-ALPHA CAN FORM A FUNCTIONAL RECEPTOR FOR IL-13. ALSO SERVES AS AN ALTERNATE ACCESSORY PROTEIN TO THE COMMON CYTOKINE RECEPTOR GAMMA CHAIN FOR IL-4 SIGNALING, BUT CANNOT REPLACE THE FUNCTION OF GAMMA-C IN ALLOWING ENHANCED IL-2 BINDING ACTIVITY (BY SIMILARITY).
CC -1- SUBUNIT: INTERLEUKIN-13 RECEPTOR IS A COMPLEX OF IL4R-ALPHA, IL13R-ALPHA, AND POSSIBLY OTHER COMPONENTS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: SPLEEN, LIVER, THYMUS, HEART, LUNG, KIDNEY, TESTIS, STOMACH, BRAIN, SKIN, AND COLON; BUT NOT SKELETAL MUSCLE.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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CC
CC EMBL; S80963; AAB50695.1; -
CC
CC MGI; MGI:105052; Il13ral.

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DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003532; Hemtopoptn_S_F2.
DR PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal.
FT SIGNAL 1 25
FT CHAIN 26 424
FT DOMAIN 26 340 INTERLEUKIN-13 RECEPTOR ALPHA-1 CHAIN.
FT TRANSMEM 341 364 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 365 424 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 37 100 IG-LIKE C2-TYPE DOMAIN.
FT DISULFID 44 93 POTENTIAL.
FT DISULFID 132 142 BY SIMILARITY.
FT DISULFID 171 183 BY SIMILARITY.
FT CARBOHYD 35 35 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 103 103 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 338 338 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 424 AA; 48402 MW; EB8330AD0C82C9F9 CRC64;

Query Match 14.2%; Score 298; DB 1; Length 424;
Best Local Similarity 25.8%; Pred. No. 3.4e-17;
Matches 108; Conservative 70; Mismatches 158; Indels 82; Gaps 21;

OY 8 IGCLTYFLIST--TPGCTSSDDEIKVNPQDEIYDPGIGLYLQMQPRLSLDFKRECT 66
Db 7 LGEELVLLMTATVGVQVAAA---TEVQPPVTVLSVSVENLCITIMTWSPEGAS--PKCT 61
OY 67 VEY-----ELKRYNIGSETWKTITIKNLHYKDFGLNKGIEAKIHTLLPMQCT-NGSEVO 120
Db 62 LNFYFHPDQDQOKKIAPF-----HRKELPLDEKICIQVQS---QCSANSESEP 108
OY 121 SSWAETTWIS-PQGIPEFKVODMOCVYYNMOYLLCSKPGIGVLLDTNLYLFYEGDL 179
Db 109 SPLVKKC--ISPPEDPESAVTELKIMHLSYMKCSWLPGRNTSPDFTLYLYWYSLE 166
OY 180 HALQCVDIKADGONIGCFPYLEAS--DYDFYICVNGSSEKPIRSSYTFPOLQNYI 236
Db 167 KSRQC-ENIRREGOHACFKLTKEPSEFHQVNOIMVADNKG--IRPSCKIVSLSTIV 223
OY 237 KPLPPLYLFTRESSCEILKWSIPGLPIPARCFYEIEIR----- 277
Db 224 KRDP-P-HIKHLLKNGALLVQKNQN-PRSCFLTYEVEVNNQTDGRHILVEEDKQCN 281
OY 278 -EDDTTL-----VTAIVENETYLKTTNEFRQLCFEYVRSKVNICYSDGIMSEWSDKQ 329
Db 282 SSSDRNMEGTSQFOLPGVLDAVYTVRVKTKNLCF-----DDNKIMSDMSEAO 331
OY 330 CMEGEDLSK-KTLRLFWLFPFGILLIYVFTGLLR-KPNTYR-----KMIPEFCD 379
Db 332 STGEKQNSTFTYTLTLTIV-FVAVAVITLLFYLRKLKIIIFPPIPDPEKIKEMFGD 388

RESULT 4
1131_HUMAN STANDARD: PRT; 427 AA.
AC P78552; Q99656; O95646;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-13 receptor alpha-1 chain precursor (IL-13R-alpha-1) (IL-13RA-1) (CD213a1 antigen).
GN IL13RA1 OR IL13RA OR IL13R.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP MEDLINE=97165986; PubMed=9013879;
RC TISSUE=Carcinoma;
RA Miloux B., Laurent P., Bonnin O., Lupker J., Caput D., Vita N.,

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CC CC FT CARBOHYD 235 235 N-LINKED (GLCNAC. . .) (POTENTIAL)
CC CC FT CARBOHYD 265 265 N-LINKED (GLCNAC. . .) (POTENTIAL)
CC CC FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL)
CC CC FT CARBOHYD 329 329 N-LINKED (GLCNAC. . .) (POTENTIAL)
CC CC FT CARBOHYD 341 341 N-LINKED (GLCNAC. . .) (POTENTIAL)
CC CC FT CONFLICT 130 130 T -> I (IN REF. 3)
CC CC FT CONFLICT 358 358 G -> D (IN REF. 3)
CC CC FT SEQUENCE 427 AA; 48759 MM; 59833BBF54107B CRC64;
SQ
Query Match 14.0%; Score 295.5; DB 1; Length 427;
Best Local Similarity 26.0%; Pred. No. 5.5e-17;
Matches 107; Conservative 63; Mismatches 169; Indels 73; Gaps 20;
QY 11 LYTFLITTEGCTSSDTEIKVNPPODEIYDPGLYGLYLQMPRLSLDHFKECTVEY- 69
   | : : : : : | : : : : | : : : : | : : : : | : : : : |
Db 10 LMAILLACGGGGGGGAAPETOPPVNLSVSENLCTVITWNPREGAS--SNCSILYF 67
QY 70 ----ELKYRNIGSGTWTITIKNLHYKDGPRDNLNGIEAKINTLPRWC-TNGSEQSSMA 124
   | : : : : : | : : : : | : : : : | : : : : | : : : : |
Db 68 SHFDKDKDKTAPETFRST-----EYPLNETICLVGS---QSTNSEKPSLIV 114
QY 125 ETTWIS-PQGIPEPTKYQMDCVYNNQYLCSMKPGISGLVDITNYNLFYVEGDHALQ 183
   | : : : : : | : : : : | : : : : | : : : : | : : : : |
Db 115 EKC--ISRPEDPRSATLELOCIMHNSLYMKSMLPGNTSPDINTLYYHNRSLERKHQ 172
QY 184 CVDYIKADGONICRFPYLEASD--YKDEYICVNGSSENKRIRSSYFTEQLONIVKPLR 241
   | : : : : : | : : : : | : : : : | : : : : | : : : : |
Db 173 C-ENIFREGGYGCSFDLTWKVDSSFEHQSVQIMKDNAGIKRPSFNIPLTSRKPPDR 231
QY 242 --VLTGTRRESSCIIKLKMSIPLRIPARCDEYIEIREDTT-----LYTAVENNTY 293
   | : : : : : | : : : : | : : : : | : : : : | : : : : |
Db 232 HIKNLSTHND--DLVQWENPQNT-SRCLTEYEVNNSQTEHNFYVQEAACEDEF 287
QY 294 TLKTNTEETROLQCFVY-----RSKVNLYTC-SDDGIMSEMSDKOCWEGEDLSKK 339
   | : : : : : | : : : : | : : : : | : : : : | : : : : |
Db 288 ERNVEN--CFNVPGLPDTLNTVTRIRKVTNKLCTYEDDKLMSMSQEM-----SICKK 339
QY 340 TLRFWLRF-----GFTLLIVIEVTGI--LLRKNPYR-KMIRPEFCD 379
   | : : : : : | : : : : | : : : : | : : : : | : : : : |
Db 340 RNSLTLYTMLLIVPVAIAIYLLVLLKRLKIIFPPIPPGKIKFEMFEGD 391
RESULT 5
PRLR_CHICK STANDARD; PRT; 831 AA.
AC 004594;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Prolactin receptor precursor (PRL-R) (CPRLP).
GN PRLR.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=white leghorn; TISSUE=Kidney;
RX MEDLINE=93075121; PubMed=1445292;
RA Tanaka M., Maeda K., Okubo T., Nakashima K.;
RT "Double antenna structure of chicken prolactin receptor deduced from
RT the cDNA sequence.";
CC Biochem. Biophys. Res. Commun. 188:490-496(1992).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
CC PROLACTIN.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -!- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC
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Db 198 TFINSGEGQAVHNGSSKRAAIKPFQDLSPALDDVNPRTNVEIESN-SLYIGWE 256
QY 260 IPLGPAPRCDFYEIEIEDD-----TTLVATVENEFTLTETMETROLCPVY 308
Db 257 KPLSAFPHCHCNELKITYNTKNGHQEKLANFKISKIDVSTYSIO-----V 305
QY 309 RSKVNYICSDGIGSEMSDKOCMEGEDISKRTLRFW---LPEGFILIVFYVTLGLLR 364
Db 306 RAAVSSPCRMGRCMGEMS-QPIYVCKE--RKSLVE-WHLIVLPFAACFVLLIF--SLICR 359
QY 365 KPNYTPKMP 374
Db 360 VCHLWTRLEP 369

RESULT 7
PRLR_MEIGA STANDARD; PRT; 831 AA.
ID PRLR_MEIGA Q91091; Q91092;
AC Q91094; Q91091; Q91092;
DT 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
De Prolactin receptor precursor (PRL-R) (TPRLR).
CN PRLR.
OS Meleagris gallopavo (Common turkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archaeoptera; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
OX NCBI_Taxid=9103;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Zhou J.F., Zadworny D., Guemene D., Kuhnlein U.;
RT "Molecular cloning, tissue distribution, and expression of the
RT prolactin receptor during various reproductive states in Meleagris
RT gallopavo."
RL Biol. Reprod. 55:1081-1090(1996).
RN [2]
RP SEQUENCE OF 82-121 AND 473-522 FROM N.A.
RC TISSUE=Ovary;
RA Plts G.R., You S.K., Foster D.N., el Halawani M.E.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBD databases.
CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
CC PROLACTIN.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -----
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CC or send an email to license@isb-sib.ch.)
CC -----
CC
DR EMBL: L76587; AAB01544.1; -
DR EMBL: U22947; AAA75038.1; -
DR EMBL: U22924; AAA75039.1; -
DR HSSP: P16471; 1BP3
DR InterPro: IPR002996; CR1A
DR InterPro: IPR003961; FN_III
DR InterPro: IPR003528; Hemtopoptn_L_F1
DR Pfam: PF00041; fn3; 4
DR SMART: SM00060; FN3; 3
DR PROSITE: PS01352; HEMATOPO_REC_L_F1; 1
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNAL 1 23
FT CHAIN 24 831 PROLACTIN RECEPTOR.
FT DOMAIN 24 438 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 439 459 POTENTIAL.
FT DOMAIN 460 831 CYTOPLASMIC (POTENTIAL).

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FT DOMAIN 25 122 FIBRONECTIN TYPE-III 1.
FT DOMAIN 123 225 FIBRONECTIN TYPE-III 2.
FT DOMAIN 228 325 FIBRONECTIN TYPE-III 3.
FT DOMAIN 326 428 FIBRONECTIN TYPE-III 4.
FT DISULFID 36 46 BY SIMILARITY.
FT DISULFID 75 86 BY SIMILARITY.
FT CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 91 91 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 112 112 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 303 303 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 315 315 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 335 335 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 831 AA; 94394 MW; 220916320F77FAC1 CRC64;

Query Match 11.38; Score 238; DB 1; Length 831;
Best Local Similarity 26.18; Pred. No. 6,7e-12;
Matches 97; Conservative 53; Mismatches 178; Indels 44; Gaps 17;

QY 18 TTFGCTSSDTEIKVN--PRODFE---IVDPC-----YLGXYLQWQPLSL 59
Db 97 TTYNITVATNEIGSNSSDPDYVDTSTVQPSPVNLTLETQRYANIMYLMAKWSPPLA 156
QY 60 DHEFCEVEYELKRYNIGSETWKTITTKNLHYKDGFDLNGKIEAKHTLLPMQCTNGSEV 119
Db 157 DASSNHLHYHLRLKPEKKEMEYV---PVGQYQCKNR-LNNGMHRVYVGRCLDPE 212
QY 120 QSSW-AETTWISPOGIPETRVQDMCVYIMWQYLLCSWKGICVLLDTNLYFTWEG 178
Db 213 WSEWSEERRILISGSLSPKPTITKCRSPKFTFCWKGGLDGHPTNLTLLYSKEGE 272
QY 179 DHALQCVDIKADONICRPREYLEASDYKDFYICVNGSSNKRIRSSYFFOLQNTYKP 238
Db 273 EGYVECPDY-RTAGPN-SCYDCKKHTSWYNTYNTKATNMGSSNDDPRHYVDTYIYOP 330
QY 239 LPVYLTFTRSSCEIK---LKWS-IPLGPIPA--RCFDYEIEIR-EDDTTLVATVEN 290
Db 331 DPPANVLTLEKRPINRKYMLTWSPPLADVRSGWMLTLDVELRKPEEGEEMETVFQ 390
QY 291 ET-YTLKTTNTROLCPYRSKVNIGSDD--GIWSESDQCKE-GEDSLKTLRLFWL 346
Db 391 QTOYKMSFLNKGKYYI-----VOIHCKPDHNGSSESNYIETPDEFVKDMI-VMI 443
QY 347 PEGFILLIVIV 358
Db 444 VLGVLSSLICLI 455

RESULT 8
CYRG_HUMAN STANDARD; PRT; 369 AA.
ID CYRG_HUMAN P31785;
AC P31785;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cytokine receptor common gamma chain precursor (gamma-C) (Interleukin-
DE 2 receptor gamma chain) (IL-2R gamma chain) (p64) (CD132 antigen).
GN IL2RG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RX MEDLINE=92335883; PubMed=16315539;
RA Takeshita T., Asao H., Ohlani K., Ishii N., Kumaki S., Tanaka N.,
RA Munakata H., Nakamura M., Sugamura K.;
RT "Cloning of the gamma chain of the human IL-2 receptor."
RL Science 257:379-382(1992).
RN [2]
RP SEQUENCE FROM N.A.

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RC TISSUE-Liver; Pubmed=8514792;  
 RX MEDLINE=9329387;  
 RA Noguchi M., Adelstein S., Cao X., Leonard W.J.;  
 RT "Characterization of the human interleukin-2 receptor gamma chain  
 gene.";  
 RL J. Biol. Chem. 268:13601-13608(1993).  
 RN [3]  
 RP SEQUENCE FROM N.A., AND VARIANTS ASP-114 AND ASN-153.  
 RX MEDLINE=94004847; Pubmed=8401490;  
 RA Puck J.M., Deschenes S.M., Porter J.C., Dutra A.S., Brown C.J.,  
 RL Willard H., Henthorn P.S.;  
 RT "The interleukin-2 receptor gamma chain maps to Xq13.1 and is mutated  
 in X-linked severe combined immunodeficiency, SCIDX1.";  
 RL Hum. Mol. Genet. 2:1099-1104(1993).  
 RN [4]  
 RP IDENTIFICATION AS A IL-4R SUBUNIT.  
 RX MEDLINE=94090315; Pubmed=8266076;  
 RA Kondo M., Takeshita T., Ishii N., Nakamura M., Watanabe S.,  
 RL Arai K.-I., Sugamura K.;  
 RT "Sharing of the interleukin-2 (IL-2) receptor gamma chain between  
 receptors for IL-2 and IL-4.";  
 RL Science 262:1874-1877(1993).  
 RN [5]  
 RP IDENTIFICATION AS A IL-4R SUBUNIT.  
 RX MEDLINE=94090317; Pubmed=8266078;  
 RA Russell S.M., Kegan A.D., Harada N., Nakamura Y., Noguchi M.,  
 RL Leland P., Friedman M.C., Miyajima A., Puri R.K., Paul W.E.,  
 RA Leonard W.J.;  
 RT "Interleukin-2 receptor gamma chain: a functional component of the  
 interleukin-4 receptor.";  
 RL Science 262:1880-1883(1993).  
 RN [6]  
 RP IDENTIFICATION AS A IL-7R SUBUNIT.  
 RX MEDLINE=94090316; Pubmed=8266077;  
 RA Noguichi M., Nakamura Y., Russell S.M., Ziegler S.F., Tsang M., Cao X.,  
 RL Leonard W.J.;  
 RT "Interleukin-2 receptor gamma chain: a functional component of the  
 interleukin-7 receptor.";  
 RL Science 262:1877-1880(1993).  
 RN [7]  
 RP 3D-STRUCTURE MODELING OF 57-248.  
 RX MEDLINE=95111955; Pubmed=7529123;  
 RA Bamorough P., Hedgecock C.J., Richards W.G.;  
 RT "Type interleukin-2 and interleukin-4 receptors studied by molecular  
 modelling.";  
 RL Structure 2:839-851(1994).  
 RN [8]  
 RP VARIANTS XSCID PHE-115; CYS-240 AND IL2-241.  
 RX MEDLINE=94130970; Pubmed=8299698;  
 RA Disanto J.P., Dautry-Varsat A., Certain S., Fischer A.,  
 RL de Saint Basile G.;  
 RT "Interleukin-2 (IL-2) receptor gamma chain mutations in X-linked  
 severe combined immunodeficiency disease result in the loss of  
 high-affinity IL-2 receptor binding.";  
 RL Eur. J. Immunol. 24:475-479(1994).  
 RN [9]  
 RP VARIANT XSCID LYS-68.  
 RX MEDLINE=94375038; Pubmed=8088810;  
 RA Markiewicz S., Subtil A., Dautry-Varsat A., Fischer A.,  
 RL de Saint Basile G.;  
 RT "Detection of three nonsense mutations and one missense mutation in  
 the interleukin-2 receptor gamma chain gene in SCIDX1 that  
 differently affect the mRNA processing.";  
 RL Genomics 21:291-293(1994).  
 RN [10]  
 RP VARIANT XSCID HIS-162.  
 RX MEDLINE=94300093; Pubmed=8027558;  
 RA Ishii N., Asao H., Kimura Y., Takeshita T., Nakamura M., Tsuchiya S.,  
 RL Kono T., Meda M., Uchiyama T., Sugamura K.;  
 RT "Impairment of ligand binding and growth signaling of mutant IL-2  
 receptor gamma-chains in patients with X-linked severe combined  
 immunodeficiency.";  
 RL J. Immunol. 153:1310-1317(1994).

RN [11]  
 RP VARIANT XSCID ASN-39.  
 RX MEDLINE=95023932; Pubmed=7937790;  
 RA Disanto J.P., Rieux-Laucat F., Dautry-Varsat A., Fischer A.,  
 RL de Saint Basile G.;  
 RT "Defective human interleukin 2 receptor gamma chain in an atypical X  
 chromosome-linked severe combined immunodeficiency with peripheral T  
 cells.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 91:9466-9470(1994).  
 RN [12]  
 RP VARIANTS XSCID CYS-226 AND HIS-226.  
 RX MEDLINE=95397841; Pubmed=7668284;  
 RA Pepper A.E., Buckley R.H., Small T.N., Puck J.M.;  
 RT "Two mutational hotspots in the interleukin-2 receptor gamma chain  
 gene causing human X-linked severe combined immunodeficiency.";  
 RL Am. J. Hum. Genet. 57:564-571(1995).  
 RN [13]  
 RP VARIANT XSCID SER-183.  
 RX MEDLINE=96013903; Pubmed=7557965;  
 RA Clark P.A., Lester T., Genet S., Jones A.M., Hendriks R.,  
 RL Levinsky R.L., Kinon C.;  
 RT "Screening for mutations causing X-linked severe combined  
 immunodeficiency in the IL-2R gamma chain gene by single-strand  
 conformation polymorphism analysis.";  
 RL Hum. Genet. 96:427-432(1995).  
 RN [14]  
 RP VARIANT XSCID 235-GLN--TRP-237 DUPL.  
 RX MEDLINE=95164726; Pubmed=7860773;  
 RA Puck J.M., Pepper A.E., Bedard P.-M., Laframboise R.;  
 RT "Female germ line mosaicism as the origin of a unique IL-2 receptor  
 gamma-chain mutation causing X-linked severe combined  
 immunodeficiency.";  
 RL J. Clin. Invest. 95:895-899(1995).  
 RN [15]  
 RP VARIANT XSCID GLN-293.  
 RX MEDLINE=95190013; Pubmed=7883965;  
 RA Schmalstieg F.C., Leonard W.J., Noguichi M., Berg M., Rudloff H.E.,  
 RL Denney R.M., Dave S.K., Brooks E.G., Goldman A.S.;  
 RT "Missense mutation in exon 7 of the common gamma chain causes a  
 moderate form of X-linked combined immunodeficiency.";  
 RL J. Clin. Invest. 95:1169-1173(1995).  
 RN [16]  
 RP VARIANT XSCID ARG-115.  
 RX MEDLINE=97042245; Pubmed=8900089;  
 RA Stephan V., Mahn V., Le Dist F., Dirksen U., Broeker B.,  
 RL Mueller-Fleckenstein I., Horneft G., Schroten H., Fischer A.,  
 RA de Saint Basile G.;  
 RT "Atypical X-linked severe combined immunodeficiency due to possible  
 spontaneous reversion of the genetic defect in T cells.";  
 RL New Engl. J. Med. 335:1563-1567(1996).  
 RN [17]  
 RP VARIANT XSCID GLN-285.  
 RX MEDLINE=97295088; Pubmed=9150740;  
 RA Jones A.M., Clark P.A., Katz F., Genet S., McMahon C., Alterman L.,  
 RL Cant A., Kinon C.;  
 RT "B-cell-negative severe combined immunodeficiency associated with a  
 common gamma chain mutation.";  
 RL Hum. Genet. 99:677-680(1997).  
 RN [18]  
 RP VARIANT XSCID CYS-222.  
 RX MEDLINE=98064061; Pubmed=9399950;  
 RA Sharfe N., Shahar M., Rolfman C.M.;  
 RT "An interleukin-2 receptor gamma chain mutation with normal thymus  
 morphology.";  
 RL J. Clin. Invest. 100:3036-3043(1997).  
 RN [19]  
 RP FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF  
 INTERLEUKINS.  
 CC -I- SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7, IL-21  
 AND PROBABLY ALSO THE IL-13 RECEPTORS.  
 CC -I- SUBCELLULAR LOCATION: TYPE I membrane protein.  
 CC -I- DISEASE: DEFECTS IN IL2RG ARE THE CAUSE OF A SEVERE COMBINED  
 IMMUNODEFICIENCY, WHICH IS KNOWN AS AGAMAGLOBULINEMIA, SWISS TYPE  
 OR X-LINKED SEVERE COMBINED IMMUNODEFICIENCY DISEASE (XSCID).

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CC -1 SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1 SIMILARITY: CONTAINS 1 FIBROBLAST TYPE III-LIKE DOMAIN.
CC -1 DATABASE: NAME=PROV; NOTE=cd guide cd132 entry".
WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd132.htm".
CC -1 DATABASE: NAME=IL2Rdbase; NOTE=X-linked SCID mutation database;
WWW="http://www.nhgrl.nih.gov/DIR/GMBA/SCID/".
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CC -----
DR EMBL: D11086; BAA01857.1; -.
DR EMBL: L12183; AAA59145.1; -.
DR EMBL: L12178; AAA59145.1; JOINED.
DR EMBL: L12176; AAA59145.1; JOINED.
DR EMBL: L12177; AAA59145.1; JOINED.
DR EMBL: L12179; AAA59145.1; JOINED.
DR EMBL: L12180; AAA59145.1; JOINED.
DR EMBL: L12181; AAA59145.1; JOINED.
DR EMBL: L12182; AAA59145.1; JOINED.
DR EMBL: L19546; AAC37524.1; -.
DR PIR: A42565; A42565.
DR PDB: 1ILM; 26-JAN-95.
DR PDB: 1ILN; 26-JAN-95.
DR GeneW: HGNC:6010; IL2RG.
DR MIM: 308380; -.
DR MIM: 300400; -.
DR InterPro: IPR002996; CRIA.
DR InterPro: IPR003961; FN_III.

- Query Match 10.5%; score 220; DB 1; Length 369;
Best Local Similarity 25.5%; Pred. No.7.5e-11;
Matches 70; Conservative 48; Mismatches 121; Indels 36; Gaps 11;

QY 97 LNKGIKAKIHLPLPQCNNGSE-VOSSNAETTYWISPGIPEITKVQMDCYVYNNQYLLC 155
Db 19 LGVGINTIILT-----PFGNEDFTADEFLTMTPTDSLVSSTILPLPEVQCFEFNENYMC 72
QY 156 SM-----KPGIGVLDTNPNLFYVEGLDH-ALQCVDIKADQNGICRPFYLEADSY 207
Db 73 TWNSSESEP-----TNLLIHTYKMSDNDKVQKCHYLESEITSGCQLQKKEIHL 125
QY 208 KDEYICVNGSSENNKIRSYTFQLONTVKPLRPVYLTFTRSSCEIKLWSIPGLPIPA 267
Db 126 QTFVVOLODPRE--PRRATQMLKLQNLVYIPAPENLTLHKLSQLELNNM---NRFLL 180
QY 268 RCFDEIETIRD-DTLYLTATYVE-NEYTTLKTNETRLQLCFVYRKSKVNIYCSDDGINSSEW 325
Db 181 HCLEHLVYRTDWDHSWTQSVDYNRKFSLSPEVDQKRTYFRVRSRFPNPLGCSAQHSEW 240
QY 326 SDKQCEGEDLSKRTLLRFWLPFGFILLVYFVTG 360
Db 241 SHPIHW-GSNTSKEN-----PFLFALNAVYISVG 268

RESULT 9
PRLR-COLLI STANDARD; PRT; 830 AA.
AC 090374;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Prolactin receptor precursor (PRL-R).
GN PRLR.
OS Columba livia (Domestic pigeon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Columbiformes; Columidae; Columba.
OX NCBI_TaxID=9932;
NM [1]

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PC SEQUENCE FROM N.A.
RP TISSUE=Cropsac:
RX MEDLINE=94283267; PubMed=7516666;
RA Chen X., Horseman N.D.;
RT "Cloning, expression, and mutational analysis of the pigeon prolactin receptor.";
RL Endocrinology 135:269-276(1994).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE PROLACTIN.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -!- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -----
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CC -----
CC EMBL: U07694; AAA20646.1; -.
DR HSPSP, P164771; IPR3.
DR InterPro: IPR002996; CRIA.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003528; Hemtopoptn_L_F1.
DR Pfam: PF00041; fn3; 4.
DR SMART: SMO0060; FN3; 4.
DR PROSITE: PS01352; HEMATOPO_REC_L_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNAL 1 23
FT CHAIN 24 830
FT DOMAIN 24 439
FT TRANSMEM 440 460
FT TRANSMEM 461 830
FT DOMAIN 25 122
FT DOMAIN 123 226
FT DOMAIN 229 326
FT DOMAIN 327 429
FT DISULFID 36 46
FT DISULFID 75 59
FT CARBOHYD 59 91
FT CARBOHYD 91 100
FT CARBOHYD 100 112
FT CARBOHYD 112 112
FT CARBOHYD 132 123
FT CARBOHYD 263 363
FT CARBOHYD 304 304
FT CARBOHYD 316 316
FT CARBOHYD 336 336
SQ SEQUENCE 830 AA; 94507 MW; 36074E83CDF69EEF CRC64;

Query Match 10.3%; Score 216.5; DB 1; Length 830;
Best Local Similarity 24.4%; Pred. No. 3.9e-10;
Matches 93; Conservative 53; Mismatches 174; Indels 61; Gaps 16;

OY 18 TTFPGCTSSDFEIKVNPQDFEYIDPGLG-----YLYQW 53
DB 97 TTYNTYVAMNEIGSS-----DPOYVDVTSIVQDPAPVNLSELTSTASTYTLAKRW 150
OY 54 QPPLSLDFHFKECTV-EYEELKYRNIGSEWAKTITFNKNLYKKGDFLNKCIETAKIHITLPMQ 112
DB 151 SPPPLADVTSNHYRYRLRLKRPKEKREMEYV---SVCVOYQYKYNR-LQAGVKTYYQVR 206
OY 113 CTNGSEVOSSNAETTYWISPGQ-IPETKVQDMDCVYVMQYLLCSWKPRGIGVLLDTFTNYL 171
DB 207 CVLDIGEMSEWSSERHIIIPNGESPEPEPTIIKCRSPKEKFTFCWKMGSGDGHPTNYTL 266
OY 172 FYWVEGDHIALQOCVDYIKADGONIGCRPRYLDELASQYKQFYICVNSSENKRIRSSYFTFQ 231
DB 267 LYSKEGGERVYECEDY-ETAGPN-SCFYDKNKHTSWTLYNTVATNTIGSNVSDPLVVD 324
OY 232 LQNIYKPLPYVLYLFTFRSSCEIK-----LKMS-IPLGIPR-RCFDVEIELREDDTLV 284

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[illegible]

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CC -I SIMILARITY: CONTAINS 1 FIBROBLAST TYPE III-LIKE DOMAIN.
CC -----
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CC -----
DR EMBL, D13821; BAA02974.1; -
DR EMBL, U21795; AAA64279.1; -
DR EMBL, D13565; BAA02760.1; -
DR EMBL, L20048; AAA39286.1; -
DR EMBL, S75852; AAB32904.1; -
DR EMBL, S75844; AAB32904.1; JOINED.
DR EMBL, S75845; AAB32904.1; JOINED.
DR EMBL, S75847; AAB32904.1; JOINED.
DR EMBL, S75848; AAB32904.1; JOINED.
DR EMBL, S75849; AAB32904.1; JOINED.
DR EMBL, S75850; AAB32904.1; JOINED.
DR EMBL, S75851; AAB32904.1; JOINED.
DR EMBL, X75337; CAA53085.1; -
DR PIR, JN0592; JN0592.
DR PIR, JN0775; JN0775.
DR HSP, P31785; IILM.
DR MGD, MGI:96551; I12FG.
DR InterPro: IPR002996; CRIA.
DR InterPro: IPR003961; FN.III.
DR InterPro: IPR003531; Hemtopopln_S.F1.
DR Pfam: PF00041; fn3; 1.
DR SMART: SM00060; FN3; 1.
DR PROSITE: PS01355; HEMATOPO_REC_S.F1; 1.
DR Receptor: Transmembrane; Glycoprotein; Signal.
KW SIGNAL 1 22 CYTOKINE RECEPTOR COMMON GAMMA CHAIN.
FT CHAIN 23 369 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 23 263 POTENTIAL.
FT TRASMEN 264 284 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 285 369 FIBROBLAST TYPE-III.
FT DISULFID 62 72 POTENTIAL.
FT DISULFID 102 115 POTENTIAL.
FT CARBOHYD 71 71 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 75 75 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 96 96 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 164 164 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 369 AA; 42241 MW; CBED5B459077AC7 CRC64;

Query Match 10.1%; Score 212.5; DB 1; Length 369;
Best Local Similarity 26.9%; Pred. No. 3,1e-10;
Matches 67; Conservative 43; Mismatches 116; Indels 23; Gaps 9;

QY 136 PETKYQMDVCYYNNQYLLCSW---KEIGVLDNTNLFYWGSDHAL--QCVDIK 189
      | : : : | : : | : : | : : | : : | : : | : : | : : | : : |
DB 53 PTLPLPEVOCYCFNIEYMNCTWNSSEPOA-----TNLTILHYRYKVSDMNTPQECSHYLF 107

QY 190 AGGQNICGFPLLEASDYDFIYICWGSSENKPIRSSYTFPOLONIVKRLPVYTLFIRE 249
      | : : : | : : | : : | : : | : : | : : | : : | : : | : : |
DB 108 SKEITSGCQIQKEDLIQYTFVQVL--QDPKPRRAVOKLMDLIVIPRADENLTLSL 165

QY 250 SSCETIKLKSIFLGPAPCFDELEIRDP--PTTLVTAVENE--VYTLKTNETPQLCFV 307
      | : : : | : : | : : | : : | : : | : : | : : | : : | : : |
DB 166 SESQQLERAK--SRHFKKGLQYIVQYRNRBRSWELVINEPRSLPSVDLAKRYTR 223

QY 308 VNSKVNITYSDGIMSEWSKDQWES---EDISKKTLLRFMLPGCF--ILILVIFVGL 361
      | : : : | : : | : : | : : | : : | : : | : : | : : | : : |
DB 224 VSRVRYPIGSSQOWSKMQPVHMGSHTVENPISLFALEAVLIPVGTGLITLLIFVYCW 283

QY 362 LARKPYTP 370
      | : : : | : : | : : | : : | : : | : : | : : | : : | : : |
DB 284 LERMPPIP 292

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RESULT 11
CYRG_CANFA
ID CYRG_CANFA STANDARD: PRT: 373 AA.
AC P40321:
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cytokine receptor common gamma chain precursor (gamma-c)
DE (Interleukin-2 receptor gamma chain) (IL-2R gamma chain) (P64).
GN IL2RG
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
ON NCBI_Taxid=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=9510114; PubMed=7829104;
RA Henthorn P.S., Somberg R.L., Fimiani V.M., Puck J.M., Patterson D.F.,
RA Felsburg P.J.;
RT "IL-2R gamma gene microdeletion demonstrates that canine X-linked
RT severe combined immunodeficiency is a homologue of the human
RT disease.";
RL Genomics 23:69-74(1994).
CC -1- FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF
CC INTERLEUKINS.
CC -1- SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7, IL-21
CC AND PROBABLY ALSO THE IL-13 RECEPTORS.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- DISEASE: DEFECTS IN IL2RG ARE THE CAUSE OF A CANINE X-LINKED
CC SEVERE COMBINED IMMUNODEFICIENCY.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
-----
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CC or send an email to license@isb-sib.ch).
-----
CC
CC EMBL: U04361; AAC48403.1; -.
CC HSSP: P31785; IILM.
CC InterPro: IPR002996; CRIA.
CC InterPro: IPR003961; FN.III.
CC InterPro: IPR003531; Hemtopoptn_S_F1.
CC SMART: SM00060; FN3; 1.
CC PROSITE: PS01355; HEMATOPO_REC_S_F1; 1.
CC Receptor: Transmembrane; Glycoprotein; signal.
FT SIGNAL 1 22
FT CHAIN 23 373 POTENTIAL.
FT DOMAIN 23 261 CYTOKINE RECEPTOR COMMON GAMMA CHAIN.
FT TRANSMEM 262 283 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 284 373 POTENTIAL.
FT DOMAIN 151 249 CYTOPLASMIC (POTENTIAL).
FT DISULFID 62 72 FIBRONECTIN TYPE-III.
FT DISULFID 102 115 POTENTIAL.
FT CARBOHYD 24 24 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 71 71 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 75 75 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 164 164 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 249 249 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 249 249 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 373 AA; 42516 MW; 03A0DEF8B089DB CRC64;
Query Match 9.9%; Score 208; DB 1; Length 373;
Best Local Similarity 26.0%; Pred. No. 7.4e-10;
Matches 69; Conservative 48; Mismatches 108; Indels 40; Gaps 12;

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QY 115 NGSE-----VOSSMAETTYWISPGIPEYKQVDMDCVYYNMWOLICSW-----KPGI 161
DQ 31 NGNEDITPDEFPLATPSET---LSVSSLPLEVO---CFVFNVEYKNCNTNMSSESRP-- 82
QY 162 GVLIDTYNINLEFYWEGL--DHALQCVDIYKADGNCNICRPPYLEASQYKPFYICVNSSE 219
DQ 83 -----TNLTLLHYWYKNSNDKRVQCGHYLFESREVTACWMLQKEIHLIYEFVQALRDPRE 137
QY 220 NKPIRSSYFETOLQNIKPLPPVYLFTRESCEIKLKWSIPLGIPARCFDEYEIRED 279
DQ 138 --PRKSTQKLIKQNLQNIYIPAPENUTLHNSSESLSEWS---NRHLDCLEHYVQYRSD 192
QY 280 -DTTLVTATVEN--ETYLKTKTNETRQLCFYVRKSNVYICSDDGIMSEWSDKQCEGEDLS 337
DQ 193 WDRSRTQSDVDRHNSFSLPSVDGKFTYFVRYSRNYNPLCSAQAGWSBSPHIM-GSNTS 251
QY 338 KKTLL-----RFWLPGFILLIVIFV 358
DQ 252 KENPLFASEAVLIPLGSMGLISLI 276

RESULT 12
IL3B_MOUSE
ID IL3B_MOUSE STANDARD: PRT: 878 AA.
AC P26954;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Interleukin-3 receptor class II beta chain precursor (colony
DE stimulating factor 2 receptor, beta 2 chain).
GN CSF2RB2 OR AIZCA OR IL3RB2 OR IL3R.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90117145; PubMed=2404337;
RA Itoh N., Yonehara S., Schreurs J., Gorman D.M., Maruyama K., Ishii A.,
RA Yahara I., Arai K., Miyajima A.;
RT Cloning of an interleukin-3 receptor gene: a member of a distinct
RT receptor gene family.";
RL Science 247:324-327(1990).
CC -1- FUNCTION: IN MOUSE THERE ARE TWO CLASSES OF HIGH-AFFINITY IL-3
CC RECEPTORS. ONE CONTAINS THIS IL-3-SPECIFIC BETA CHAIN AND THE
CC OTHER CONTAINS THE BETA CHAIN ALSO SHARED BY HIGH-AFFINITY IL-5
CC AND GM-CSF RECEPTORS.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
-----
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-----
CC
CC EMBL: M28655; AAA39295.1; -.
CC PIR: A40091; A40091.
CC MGD: MGI:1339760; Csf2rb2.
CC InterPro: IPR002996; CRIA.
CC InterPro: IPR000282; Cytok receptor_2.
CC InterPro: IPR003961; FN.III.
CC InterPro: IPR003531; Hemtopoptn_S_F1.
CC Pfam: PF00041; FN3; 2.
CC SMART: SM00060; FN3; 2.
CC PROSITE: PS01355; HEMATOPO_REC_S_F1; 1.
CC Receptor: Transmembrane; Glycoprotein; signal.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 878 INTERLEUKIN-3 RECEPTOR CLASS II BETA
FT CHAIN CHAIN.

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FT DOMAIN 23 440 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 461 462 POTENTIAL.
FT DOMAIN 463 878 CYTOPLASMIC (POTENTIAL).
FT DISULFID 39 49 BY SIMILARITY.
FT DISULFID 78 95 BY SIMILARITY.
FT DISULFID 254 264 BY SIMILARITY.
FT DISULFID 293 310 BY SIMILARITY.
FT CARBOHYD 62 62 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 878 AA; 97195 MW; 8BEC9092ADC24D56 CRC64;

Query Match 9.3%; Score 195; DB 1; Length 878;
Best Local Similarity 24.1%; Pred. No. 2.5e-08;
Matches 86; Conservative 59; Mismatches 150; Indels 62; Gaps 23;

QY 34 PRODFELVDGVLGYLQWQPL---SLDHFECTVEYEELKYNISSEYTKITITKRLH 90
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
139 PPKDIHISPSG--DHFLEMSVSLGDSQVSWLSKSDIEFEVAVYRL--QDSMED--ASSLH 193
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
91 YKDFDINKGIEAKIHTLLP-----MOCINGSEVO---SSMAETTYWISPOGIPET 138
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
194 -TSNFQVN--LEPKL--FLPMSITAAKVRTRLSSGSSLSGKSPKSWSPKSHVMDSPG-DKA 247
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 139 KYVDMDCVYNNMVOYLCSMKRPGICVLLDTYNNLFYWEGLDHALQCVYIKADQONT--- 195
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
248 QPOMLOCFPGDIOISLHCSMEVMTQTGVSFGFLYRPSAPAEKSCPVNKEPQASYTR 307
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 196 -GCFFPLEASDYKDFYICVNGSSEKPIRSSYTFPOLQNVKRLPYV--LTFRESCE 253
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
PB 308 YRCSLPPEPSAHQYVSVKHLRQKFI--MSYHIQME-----PPLNQTKNRDS--- 357
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 254 IKLKMSIPLGPAPCFD--YEIEIRDDDTLVATVEN---ETYLTKTNETROCFEV 307
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 358 YSLHMEQKIP---KYIDHTFOVQYKKKSESKMKSKEINLGRVSMPLPOLEPTSTICAR 414
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 308 VRSA--VAIYCSDDGIMSEMSDKQCEGEDLSKTKLLRPLWPGFILLIVIVTGLL 363
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 415 VVRVPSIDY--DGIMSEMSNETWT--TDWVMPYL--WI---VLLIVELIFILL 460
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 13
CYRG_BOVIN STANDARD; PRT; 379 AA.
ID CYRG_BOVIN STANDARD; PRT; 379 AA.
AC 095118;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cytokine receptor common gamma chain precursor (gamma-C)
DE (Interleukin-2 receptor gamma chain) (IL-2R gamma chain) (P64).
GN IL2RG.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96268473; PubMed=8672241;
RA Yoo J., Stone R.T., Solinas-Toldo S., Fries R., Beattie C.W.;
RT Cloning and chromosomal mapping of bovine Interleukin-2 receptor
RT gamma gene."
RL DNA Cell Biol. 15:453-459(1996).
CC -1- FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF
CC INTERLEUKINS.
CC -1- SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7, IL-21
CC AND PROBABLY ALSO THE IL-13 RECEPTORS.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
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CC -----
DR EMBL; U33748; AB07812.1; -.
DR HSSP; P31785; IILM.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003531; Hemtopoptn_S_F1.
DR Pfam; PF00041; Fn3; 1.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 379 CYTOKINE RECEPTOR COMMON GAMMA CHAIN.
FT DOMAIN 23 269 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 270 290 POTENTIAL.
FT DOMAIN 291 379 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 158 256 FIBRONECTIN TYPE-III.
FT DISULFID 68 78 POTENTIAL.
FT DISULFID 109 122 POTENTIAL.
FT CARBOHYD 77 77 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 81 81 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 171 171 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 379 AA; 43037 MW; 33CFAD9C9B032178 CRC64;

Query Match 9.0%; Score 189.5; DB 1; Length 379;
Best Local Similarity 26.2%; Pred. No. 2.5e-08;
Matches 62; Conservative 42; Mismatches 106; Indels 27; Gaps 9;

QY 135 IPEKVDMDCVYNNMVOYLCSW-----KPGICVLLDTYNNLFYWE---EGLDHALQCV 185
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 61 LPLPKVQ--CFEYNNVEYMCNTWNSSEPOP-----NNLTLYGYRNFNGDKLQECG 110
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 186 DYKADQONICRPPYLEASDYKDFYICVNGSSEKPIRSSYTFPOLQNVKRLPYVLT 245
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 111 HYLSEGITSCWFKGKEIRLETFFVQLODPREHR--KQKQMLKLDVLIYAPAPENLT 168
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 246 FTRESCEIKLKMSIPLGPAPCFDYEIEIRD--DTLVATVEN--ETYLTKTNETRQ 303
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 169 LRNLSEFOLSLMS---NRYLDHCLHLVGYRSDRSRWSWTQSDVHHSFLPSVDQKL 225
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 304 LCFYVRKSVNIYCSDDGIMSEMSDKQCEGEDLSKTKLLRPLWPGFILLIVIVTGL 360
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 226 YTFVRSRYNPLCSDAQMWSMYSPIHW--GSNTSKENIENPENSFLALEAVLIPLG 281
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 14
CYRG_HUMAN STANDARD; PRT; 897 AA.
ID CYRG_HUMAN STANDARD; PRT; 897 AA.
AC P32927;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cytokine receptor common beta chain precursor (CDW131 antigen).
DE CSF2RB OR IL3RB OR IL3RB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91088571; PubMed=1702217;
RA Hayashida K., Kitamura T., Gorman D.M., Arai K., Yokota T.,
RA Miyajima A.;
RT "Molecular cloning of a second subunit of the receptor for human
RT granulocyte-macrophage colony-stimulating factor (GM-CSF):
RT reconstitution of a high-affinity GM-CSF receptor."
RL Proc. Natl. Acad. Sci. U.S.A. 87:9655-9659(1990).
RN [2]

```

RP REVISION TO 454.  
 RA Kitamura T.;  
 RL Submitted (Feb-1991) to the EMBL/Genbank/DBJ databases.  
 CC -1- FUNCTION: HIGH AFFINITY RECEPTOR FOR INTERLEUKIN-3, INTERLEUKIN-5  
 CC AND GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR.  
 CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BETA  
 CC CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.  
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  
 CC -1- DATABASE: NAME=PRO; NOTE=CD guide CDw131 entry;  
 CC WWW="http://www.ncbi.nlm.nih.gov/row/cd/cdw131.htm".  
 CC  
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 CC  
 CC EMBL: M59941; AAA18171.1; -  
 CC PIR: A39255; A39255.  
 CC HSSP: P19235; 1EBA.  
 CC Genew: HGNC:2436; CSF2RB.  
 CC MIM: 138981; -  
 CC InterPro: IPR002996; CRIA.  
 CC InterPro: IPR000282; Cytok\_receptor\_2.  
 CC InterPro: IPR003961; FN.III.  
 CC InterPro: IPR003531; Hemtopoptn\_S\_Fl.  
 CC Pfam: PF00041; Fn3; 2.  
 CC SMART: SM00060; FN3; 2.  
 CC PROSITE: PS01355; HEMATOPO\_REC\_S\_Fl; 1.  
 CC Receptor: Transmembrane; Glycoprotein; Repeat; Signal.  
 CC STGNL 1 16  
 CC CHAIN 17 897  
 CC DOMAIN 17 443  
 CC TRANSMEM 444 460  
 CC FT DOMAIN 461 897  
 CC FT DOMAIN 129 238  
 CC FT DOMAIN 336 434  
 CC FT DISULFID 35 45  
 CC FT DISULFID 75 91  
 CC FT CARBOHYD 58 58  
 CC FT CARBOHYD 191 191  
 CC FT CARBOHYD 346 346  
 CC SEQUENCE 897 AA; 97335 MW; 3398E37EDB8F393A CRC64;  
 CC  
 CC Query Match 8.5%; Score 178.5; DB 1; Length 897;  
 CC Best Local Similarity 22.5%; Pred. No. 5; 8e-07;  
 CC Matches 89; Conservative 57; Mismatches 144; Indels 105; Gaps 21;  
 CC  
 CC 32 VNPQDEIYDPGLGY-----LYLQWOP-----LSLDF----- 62  
 CC 97 VIPCQSVVVDVYFSQPDRPLSTRLLTVLTHQVOPRPRDIOISTDOHFLTLWSVAL 156  
 CC 63 -----KCTVEYELKYNIGSETWK--TIITKNLYKDGDFLNGIE-----A 103  
 CC 157 GSPQSHWLSFGDLEFVVYRL-QDSMEDAAILLSTNS-----QATIGPEHMLSSYYVA 210  
 CC 104 KIRP-LPPOCTNGSEVOSSAETTYWISPOGIPETVVOVMDCVYVWQYLLCSWKPQIG 162  
 CC 211 RVTRRLAPGSRSLRS--PSKWSPEVCWDSOPG-DEAOPNLECFDGAAYVLSCEWEVKE 267  
 CC 163 VLDLTNLYLFWYEGDLHALQCVYIKADQNG-----CRPYLEASDKKFFYCVN 215  
 CC 268 VASVSVGLTKSPDAGEECSPVLR---EGDSLFTRHHCQIPVDPATHGOYIVSVQ 324  
 CC 216 GSSENKIRSSYFTFOQNIKPLRPVYLTFTRESCEIKLWISIPGIPARCFDEIE 275  
 CC 325 PRAEKIKKSV-----NI-QMAPPSLVNTKGD-SYSLRWETMKMKREHIDHTFEIQ 375  
 CC 276 IREDDTLVAT-VENETYLTKTTN-----ETROLGFV-VRSKVNIYCSDDGIMSE 324

DB 376 YRKD-----TATWDSKTEFLQNAHSMALPALPESTRYMARVVRTSRTGY---NGIMSE 427  
 QY 325 WSDKQCEWGEDLSKTLRLRWLPFGILLIVITV 359  
 DB 428 WSEARSWDETSV-----LPMWVALIVIFLT 453  
 RESULT 15  
 CYRB\_MOUSE  
 ID CYRB\_MOUSE STANDARD; PRT; 896 AA.  
 AC P26955;  
 DT 01-OCT-1993 (Rel. 27, Created)  
 DT 01-OCT-1993 (Rel. 27, last sequence update)  
 DT 15-JUN-2002 (Rel. 41, last annotation update)  
 DE Cytokine receptor common beta chain precursor.  
 GN CSF2RB OR CSF2RBL OR ALC2B OR IL3RBL.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90319131; PubMed=1695379;  
 RA Gorman D.M., Itoh N., Kitamura T., Schreurs J., Yonehara S.,  
 RA Yahara I., Arai K., Miyajima A.;  
 RT "Cloning and expression of a gene encoding an interleukin 3 receptor-  
 RT like protein: identification of another member of the cytokine  
 RT receptor gene family".  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:5459-5463(1990).  
 CC -1- FUNCTION: HIGH AFFINITY RECEPTOR FOR INTERLEUKIN-3, INTERLEUKIN-5  
 CC AND GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR.  
 CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BETA  
 CC CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.  
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC at the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL: M34397; AAA37204.1; -  
 CC PIR: A35782; A35782.  
 CC MGD: MGI:1339759; Csf2rb1.  
 CC DR InterPro: IPR002996; CRIA.  
 CC DR InterPro: IPR000282; Cytok\_receptor\_2.  
 CC DR InterPro: IPR003531; Hemtopoptn\_S\_Fl.  
 CC PROSITE: PS01355; HEMATOPO\_REC\_S\_Fl; 1.  
 CC Receptor: Transmembrane; Glycoprotein; Repeat; Signal.  
 CC STGNL 1 22  
 CC CHAIN 23 896  
 CC DOMAIN 23 441  
 CC TRANSMEM 442 463  
 CC FT DOMAIN 464 896  
 CC FT DOMAIN 132 241  
 CC FT DOMAIN 343 440  
 CC FT DISULFID 39 49  
 CC FT DISULFID 77 94  
 CC FT CARBOHYD 62 62  
 CC FT CARBOHYD 141 141  
 CC FT CARBOHYD 350 350  
 CC SEQUENCE 896 AA; 99111 MW; 8CE16EDFDC07A959 CRC64;  
 CC  
 CC Query Match 8.2%; Score 173.5; DB 1; Length 896;  
 CC Best Local Similarity 20.7%; Pred. No. 1; 5e-06;  
 CC Matches 81; Conservative 69; Mismatches 185; Indels 57; Gaps 18;  
 CC 5 CLAIGCLYFLISTTFCGTS-----SSDTEIK-----VNPQDEIYDPGLGY 48

```
Db 94 CVPRRCVAPY---TRFSITNEDYYSFRPDSDLGIQLMWPLAQNVOPLPKNVSISSSEDR 150
QY 49 LYLOMOPPL---SLDHEKCEVEYEELKRNIGSETWKTITTKN-----LHKDGFDLNKG 100
Db 151 FLEMSVSLGDAQVSWLSSKDIEFEVAYKRL-ODSWEDAYSLHTSKFQVNEPEPKLFLPNS 209
QY 101 IEA-KIHT-LLPMOCTNGSEVOSSMAETTYWISPOGIPETKVODMDCVYNNMOYLLCSMK 158
Db 210 IYAPRVRTRLYFGSSLSGR--PSRKSPEAHMDSQPG-DKAQPONLQCFDFDGIQSLHCSWE 266
QY 159 PGIGVLLDTNNLFFYWEGLDHALQCVDIK-ADGQNI---GCRFPYLEASDYKDFYIC 213
Db 267 VMTQTTGSVSFGLFYRPSVAPAEKCSPVKPEPGASVYTRYHCSLPVPEPSAHSQYTVS 326
QY 214 VNGSSENKPIRSSYFTFOLQNIIVKPLPPVYLTFTRESSCEIKLWSIPLGPIPARCFDYE 273
327 V-----KHLQGRKIMSYNHIOMEPPTLNLTKNRDS---YSLHWETQKMAYSFIEHTFQ 377
274 IEIREDPTTLVTATVEN--ETYTLLKTNETRQLCFVRSKVINYCSDDGIMSEMSDKQGW 331
Db 378 VOYKKKSDSWEDSKTENIDRAHSMDSLQLEPDTSTICARVRVKPISNYDGIMSKWSEETW 437
QY 332 EGEDLSKRTLLRFWLPFGFILILVIFVTGLL 363
Db 438 K-TDWMVPTL--WI---VLIVFLILITLLL 461
```

Search completed: January 24, 2003, 19:36:39  
job time : 17 secs

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GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 24, 2003, 19:31:49 ; Search time 37 Seconds  
(without alignments)  
1368.520 Million cell updates/sec

Title: US-09-714-792a-4  
Perfect score: 2104  
Sequence: 1 MAFVCLAIICLYFLISTTF.....LLLRKPNTYPKMIFECDT 380

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Archived: 908470 seqs, 133250620 residues  
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: /SID52/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:\*  
2: /SID52/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*  
3: /SID52/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:\*  
4: /SID52/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:\*  
5: /SID52/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:\*  
6: /SID52/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:\*  
7: /SID52/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:\*  
8: /SID52/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:\*  
9: /SID52/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:\*  
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11: /SID52/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:\*  
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22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*  
23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2104	100.0	380	AAW24972	Human interleukin-
2	2104	100.0	380	AAW35295	Human IL-13 bindin
3	2104	100.0	380	AAW36613	Human zcytor2 cyto
4	2104	100.0	380	AAW41520	Human HR-1 recepto
5	2104	100.0	380	AAW41502	Human cytokine/pep
6	2104	100.0	380	AAW33603	Homo sapiens HR-1
7	2104	100.0	380	AAW35296	IL-13 binding chai
8	2104	100.0	380	AAW63812	Amino acid sequenc
9	2104	100.0	380	AAW72136	Human interleukin
10	2104	100.0	380	AAW29748	Human IL-13 recept

11	2104	100.0	380	AAW49201	Human IL-13R alpha
12	2078	98.8	380	AAW36614	Human zcytor2 cyto
13	1853	88.1	372	AAW36616	Celebous macaque zc
14	1764	83.8	317	AAE13746	Human soluble cyto
15	1753	83.3	315	AAW56261	Mature interleukin
16	1753	83.3	359	AAW56260	Construct containi
17	1503	71.4	386	AAW69135	Canine interleukin
18	1452.5	69.0	365	AAW69136	Canine interleukin
19	1392.5	66.2	318	AAW69137	Canine IL-13R exte
20	1382.5	66.2	561	AAW69138	Canine IL-13R alph
21	1392.5	66.2	561	AAW69141	Canine IL-13R alph
22	1392.5	66.2	563	AAW69140	Canine IL-13R alph
23	1392.5	66.2	565	AAW69139	Canine IL-13R alph
24	1194.5	56.8	383	AAW35294	Murine IL-13 bindi
25	1194.5	56.8	383	AAW35295	IL-13 binding chai
26	1194.5	56.8	383	AAW72135	Murine interleukin
27	1194.5	56.8	383	AAW29747	Mouse IL-13 recept
28	935.5	44.5	255	AAW69134	Canine interleukin
29	626.5	29.8	145	AAW69133	Canine interleukin
30	456	21.7	157	AAW56252	Interleukin-13 bin
31	311.5	14.8	366	AAW22216	Sequence of human
32	311.5	14.8	396	AAW22220	Sequence of secret
33	311.5	14.8	420	AAW22219	Sequence of secret
34	311.5	14.8	420	AAW82842	Human interleukin-
35	310.5	14.8	421	AAW25064	Human IL-5 recepto
36	305.5	14.5	430	AAW22215	Sequence of human
37	302.5	14.4	405	AAW69132	Canine interleukin
38	297	14.1	313	AAW21856	Protein used in pr
39	296	14.1	426	AAW09821	Mouse interleukin-
40	295.5	14.0	427	AAW24973	Human interleukin-
41	295.5	14.0	427	AAW19807	Human interleukin-
42	294.5	14.0	426	AAW09807	Human interleukin-
43	292.5	13.9	1026	AAW70121	IL5-R-GDP 130 fusi
44	292	13.9	335	AAW25063	Soluble human IL-5
45	292	13.9	335	AAW33699	shIL-5R-alpha. Sy

## ALIGNMENTS

RESULT 1  
AAW24972  
ID AAW24972 standard; protein; 380 AA.  
XX  
AC AAW24972;  
XX  
DT 22-JUN-1998 (first entry)  
XX  
DE Human interleukin-13 beta receptor.  
XX  
KW Interleukin-13 receptor; diagnosis; inflammation; allergy; IL-13.  
XX  
OS Homo sapiens.  
XX  
PN W09720926-A1.  
XX  
PD 12-JUN-1997.  
XX  
PF 07-NOV-1996; 96WO-FR01756.  
XX  
PR 06-DEC-1995; 95FR-0014424.  
XX  
PA (SNFI ) SANOFI SA.  
XX  
PI Caput D, Ferrara P, Laurent P, Vltá N;  
XX  
DR WPI: 1997-319773/29.  
XX  
DR N-PSDB; AAT85826, AAT86464.  
XX  
PT New purified human interleukin-13 receptors - and related nucleic  
PT acids, useful for diagnosis and treatment of inflammation, allergy,  
PT etc

PS Claim 1; Figure 2a; 83pp; French.  
XX  
CC This sequence represents interleukin-13 (IL-13) beta receptor. The  
CC invention relates to new purified peptides comprising 380 or 427 amino  
CC acid sequences, which are receptors for interleukin-13 (IL-13); the 380  
CC and 427 aa proteins are designated IL-13R beta and alpha respectively.  
CC The IL-13R beta has high affinity for IL-13 while IL-13R alpha has low  
CC affinity, but acquires high affinity when associated with the IL-4  
CC receptor. Nucleic acids encoding IL-13R beta and alpha are used as  
CC diagnostic probes to identify aberrant synthesis or genetic anomalies  
CC such as loss of heterozygosity and rearrangements, or chromosomal  
CC anomalies. They are also used for production of recombinant IL-13R beta  
CC and alpha which can be used as IL-13 antagonists, specifically to  
CC regulate IL-13-induced responses for treatment of inflammation and  
CC allergy. IL-13 receptors are also useful as antisense molecules for gene  
CC therapy (blocking synthesis of IL-13R). Antibodies are used (in standard  
CC immunoassays) to diagnose diseases associated with abnormal expression  
CC of IL-13 receptors; when coupled to a toxin also for treatment of  
CC overproduction of IL-13R. Cells that express IL-13R at the surface are  
CC used to identify ligands and modulators of IL-13R. Note: IL-13R beta  
CC is encoded by the nucleic acid sequence shown in Figure 2a in the  
CC specification (AAT86464), which is not the same as that shown in the  
CC sequence listing (AAT85828).

XX Sequence 380 AA:

Query Match 100.0%; Score 2104; DB 18; Length 380;  
Best Local Similarity 100.0%; Pred. No. 2e-197;  
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLAIGCLYFLISTFTGCTSSDTEIKVNPDPDFIVDPGYLYLQWQPLSLD 60  
Db 1 MAFVCLAIGCLYFLISTFTGCTSSDTEIKVNPDPDFIVDPGYLYLQWQPLSLD 60  
QY 61 HFKCTVEYELKRYNIGSEMTKTIITNLRHKDGFDLNKGIEAKIHLLPWOCTNSSEVQ 120  
Db 61 HFKCTVEYELKRYNIGSEMTKTIITNLRHKDGFDLNKGIEAKIHLLPWOCTNSSEVQ 120  
QY 121 SSNAETTYWISPOGIPETKQVDMDCVYNNQYLLCSMKPGIGVLDLTNYNLFWEGLDH 180  
Db 121 SSNAETTYWISPOGIPETKQVDMDCVYNNQYLLCSMKPGIGVLDLTNYNLFWEGLDH 180  
QY 181 ALOCVDYIKADGONIGCRFPYLEASDYKDRFYICVNGSSENKPIRSSYFTFOLQNIKPLP 240  
Db 181 ALOCVDYIKADGONIGCRFPYLEASDYKDRFYICVNGSSENKPIRSSYFTFOLQNIKPLP 240  
QY 241 PVLTFPTRESCEIKLKWSPILGPIPARCFDEIREDDTTLVATVENVETYLKTTNE 300  
Db 241 PVLTFPTRESCEIKLKWSPILGPIPARCFDEIREDDTTLVATVENVETYLKTTNE 300  
QY 301 TROLCFVVRKVNITYCSDDGIMSEMSDKOCWEGEDLSKTLRLRFLPFGFLLIVIVTG 360  
Db 301 TROLCFVVRKVNITYCSDDGIMSEMSDKOCWEGEDLSKTLRLRFLPFGFLLIVIVTG 360  
QY 361 LLLRKPNTYPRKMIPEFCDT 380  
Db 361 LLLRKPNTYPRKMIPEFCDT 380

RESULT 2

AAW35295  
ID AAW35295 standard; Protein: 380 AA.

AC AAW35295;

DT 27-MAR-1998 (first entry)

DE Human IL-13 binding chain of the IL-13 receptor.

KM Interleukin-13; IL-13; interleukin-13 receptor binding chain; IL-13bc;  
KW mediator; IL-13 receptor binding inhibition; IgE-mediated condition;  
KW allergy; asthma; immune complex disorder.

XX  
XX

OS Homo sapiens.

XX Key Location/Qualifiers  
FH Peptide 1..25  
FT /label= signal\_sequence  
FT /note= "putative"  
FT Protein 26..380  
FT /label= mature\_protein  
FT Domain 26..341  
FT /label= extracellular\_domain  
FT Domain 342..362  
FT /label= transmembrane\_domain  
FT Domain 363..380  
FT /label= intracellular\_domain

PN W09731946-A1.

PD 04-SEP-1997.

XX 28-FEB-1997; 97MO-U503124.

XX 01-MAR-1996; 96US-0609572.

XX (GEMV ) GENETICS INST INC.

XX Collins M, Donaldson D, Filtz L, Neben T, Whilters M;  
PI Wood C;  
XX WPI; 1997-448632/41.

DR N-PSDB; AAT95214.

XX New nucleic acid encoding interleukin-13 receptor binding chain and  
PT transformed cells - proteins, antibodies and inhibitors, for  
PT treating immunoglobulin E-mediated diseases, e.g. Graves disease,  
PT and in diagnosis

PS

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|||||
Db 181 ALQCVDIKADGONIGCRFPYLEASDYKDFYICVNGSSSEKPIRSSYFTFQLONIYKPLP 240
QY 241 PVLFTFTRESSCEIKLWMSIPLGPIPARCFDYEIEIREDDTTLVATVENEYTLKTNE 300
Db 241 PVLFTFTRESSCEIKLWMSIPLGPIPARCFDYEIEIREDDTTLVATVENEYTLKTNE 300
QY 301 TROLCFVVRASKVNIYCSDGIMSEMSDKOCWGEDLSKTKTLRFMLPFGFILLIVFYVG 360
Db 301 TROLCFVVRASKVNIYCSDGIMSEMSDKOCWGEDLSKTKTLRFMLPFGFILLIVFYVG 360
QY 361 LLRRKPNITYPKMIPEFCDT 380
Db 361 LLRRKPNITYPKMIPEFCDT 380

RESULT 3
AAM36613
AAM36613 standard; Protein: 380 AA.
AC AAM36613;
DT 30-MAR-1998 (first entry)
XX Human zcytor2 cytokine receptor protein.
DE Cytokine receptor; ligand binding; testicular cell; spermatogenesis;
KM infertility; antagonist; contraceptive; diagnostic; therapeutic.
XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT Domain 340..363
FT Domain /label= transmembrane_domain
FT Domain 364..380
FT Domain /label= intracellular_domain
FT Domain 25..339
FT Domain /label= ligand_binding_domain
XX
XX W09733913-A1.
XX 18-SEP-1997.
XX 12-MAR-1997; 97MO-US04043.
XX 13-MAR-1996; 96US-0013345.
XX (ZYMO ) ZYMOGENETICS INC.
XX Baumgartner JW, Farrah TM, Foster DC, Grant FJ;
PI O'hara FJ;
XX WPI: 1997-470820/43.
XX N-PSDB: AAT96782.
XX
XX New nucleic acid encoding testis-specific cytokine receptor - useful
XX for identification of ligands or antagonists, potentially for use as
XX male contraceptives or for infertility treatment
XX
XX Claim 2: Page 47-48; 79pp; English.
XX
XX This sequence represents a novel ligand-binding receptor, zcytor2,
XX which shares homology with cytokine receptors and was isolated from human
XX placental polyA+ RNA. The resulting polypeptide is a receptor for
XX cytokines (particularly interleukin-13) and is expressed on the surface
XX of testicular cells, probably being involved in spermatogenesis. It can
XX be used to detect ligands that promote proliferation and/or
XX differentiation of such cells in cultures and may also be used to treat
XX infertility. Antagonists of this receptor may be used to characterise
XX ligand-receptor interactions and as male-specific contraceptives. By
XX blocking the action of IL-13, receptor antagonists and ligand-binding
XX this receptor can also be used to modulate immune function, e.g. in
XX allergy and asthma, as a diagnostic to determine circulating levels of

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CC ligand and also to isolate and purify ligands. Antibodies can be used to
CC assay circulating receptor (an abnormal level may be indicative of
CC disease such as cancer), for labelling cells that express the receptor,
CC and therapeutically as antagonist.
XX
SQ Sequence 380 AA;
Query Match 100.0%; Score 2104; DB 18; Length 380;
Best Local Similarity 100.0%; Pred. No. 2e-197;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MAFVCLAIQCLTYTFLISTFTFGCTSSDTEIKVNPQDFEIVDPGYLYLOMOPPLSD 60
Db 1 MAFVCLAIQCLTYTFLISTFTFGCTSSDTEIKVNPQDFEIVDPGYLYLOMOPPLSD 60
QY 61 HREKCTVEYELKRYNIGSETWTKTITKNIHYVDGFDLNGKIEAKIHTLLPMQCTNGSEVO 120
Db 61 HREKCTVEYELKRYNIGSETWTKTITKNIHYVDGFDLNGKIEAKIHTLLPMQCTNGSEVO 120
QY 121 SSWAETTYWISPOGIPETKVDMDCVYVMQYLLCSMRKGTGLVLLDTNINLFYWEGLDH 180
Db 121 SSWAETTYWISPOGIPETKVDMDCVYVMQYLLCSMRKGTGLVLLDTNINLFYWEGLDH 180
QY 181 ALQCVDIKADGONIGCRFPYLEASDYKDFYICVNGSSSEKPIRSSYFTFQLONIYKPLP 240
Db 181 ALQCVDIKADGONIGCRFPYLEASDYKDFYICVNGSSSEKPIRSSYFTFQLONIYKPLP 240
QY 241 PVLFTFTRESSCEIKLWMSIPLGPIPARCFDYEIEIREDDTTLVATVENEYTLKTNE 300
Db 241 PVLFTFTRESSCEIKLWMSIPLGPIPARCFDYEIEIREDDTTLVATVENEYTLKTNE 300
QY 301 TROLCFVVRASKVNIYCSDGIMSEMSDKOCWGEDLSKTKTLRFMLPFGFILLIVFYVG 360
Db 301 TROLCFVVRASKVNIYCSDGIMSEMSDKOCWGEDLSKTKTLRFMLPFGFILLIVFYVG 360
QY 361 LLRRKPNITYPKMIPEFCDT 380
Db 361 LLRRKPNITYPKMIPEFCDT 380

RESULT 4
AAM41520
ID AAM41520 standard; Protein: 380 AA.
XX
XX AAM41520;
AC AAM41520;
XX
XX 22-JUN-1998 (first entry)
XX Human HR-1 receptor.
XX
XX HR-1 receptor; human; cytokine; infection; asthma; allergy;
XX haematopoietic disorder; tumour; therapy; diagnosis.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..21
XX Protein /label= Sig_peptide
XX Protein 22..380
XX Protein /label= Mat_protein
XX
XX W09747741-A1.
XX 18-DEC-1997.
XX 12-JUN-1996; 96MO-US10262.
XX 12-JUN-1996; 96MO-US10262.
XX (HUMA-) HUMAN GENOME SCI INC.
XX (SMIK ) SMITHKLINE BEECHAM CORP.
XX
XX Appelbaum ER, Hu J;
PI

```

xx WP1: 1998-052308/05.  
 DR N-PSDB: AAV04131.  
 xx Nucleic acid sequence encoding human cytokine peptide hormone  
 PT receptor - useful to treat, prevent or diagnose, e.g. lowered  
 PT resistance to infection, asthma, allergy or haematopoietic disease  
 xx  
 PS Claim 13: Page 62-64: 76pp: English.  
 CC This protein comprises a novel human cytokine/peptide hormone  
 CC receptor, designated the HR-1 receptor, that shows 27% identity  
 CC and 52% similarity to the Interleukin-5 receptor. Its amino acid  
 CC sequence was deduced from a cDNA clone (see AAV04131) obtained from a  
 CC human testis library. Recombinant HR-1 receptor can be expressed  
 CC in claimed host cells, and used in a claimed method for identifying  
 CC compounds which bind to, and activate or inhibit, it. HR-1  
 CC receptor activators and agonists can be used to treat, prevent or  
 CC diagnose predisposition to lowered resistance to infection, asthma,  
 CC allergic or haematopoietic disorders, e.g. where induced by AIDS,  
 CC aplastic anaemia, neutropenia or cytotoxic treatments for cancer.  
 CC HR-1 antagonists, e.g. antibodies or HR-1 receptor fragments, can  
 CC be used to treat conditions associated with HR-1 receptor  
 CC overexpression. The antibodies can also be used to determine HR-1  
 CC receptor levels, since overexpression may be diagnostic of tumours.  
 CC  
 xx Sequence 380 AA:  
 Query Match 100.0%; Score 2104; DB 19; Length 380;  
 Best Local Similarity 100.0%; Pred. No. 2e-197;  
 Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 50  
 QY 1 MAFVCLAIGCLYTLFLISTFTGCTSSDTEIKVNPQDFEIVDPGYLYLQWQPPSLD 60  
 DB 1 MAFVCLAIGCLYTLFLISTFTGCTSSDTEIKVNPQDFEIVDPGYLYLQWQPPSLD 60  
 QY 61 HFECTVEYELKYNIGSETWTKTITTKNLHYKDGFDLKKGIKAKHTLLPMQCTNGSEVQ 120  
 QB 61 HFECTVEYELKYNIGSETWTKTITTKNLHYKDGFDLKKGIKAKHTLLPMQCTNGSEVQ 120  
 QY 121 SSMATTYTWISPOGIPETKVDMDCVYNNMQYLCSMKPGIGVLDNTYNLFWYEGIDH 180  
 DB 121 SSMATTYTWISPOGIPETKVDMDCVYNNMQYLCSMKPGIGVLDNTYNLFWYEGIDH 180  
 QY 181 ALOCVDYTKADGONIGCFPPYLEASDYKDFYICVNGSSENKPIRSSYTFPOLQNTVPLP 240  
 DB 181 ALOCVDYTKADGONIGCFPPYLEASDYKDFYICVNGSSENKPIRSSYTFPOLQNTVPLP 240  
 QY 241 PYYLFTRESSCEIKLKWISIPGPIPARCFDEIRREDDTLVTAIVENETYLKTINE 300  
 DB 241 PYYLFTRESSCEIKLKWISIPGPIPARCFDEIRREDDTLVTAIVENETYLKTINE 300  
 QY 301 TROLCEFVVRSKVNYICSDGIMSEWSKQCGEGEDLSKKTLLRFLPGLFLLIVFVNG 360  
 DB 301 TROLCEFVVRSKVNYICSDGIMSEWSKQCGEGEDLSKKTLLRFLPGLFLLIVFVNG 360  
 QY 361 LLRKRPNTYPKMIPPEFCDT 380  
 DB 361 LLRKRPNTYPKMIPPEFCDT 380  
 RESULT 5  
 ID AAM41502 standard; Protein: 380 AA.  
 AC AAM41502;  
 DT 08-JUN-1998 (first entry)  
 DE Human cytokine/peptide receptor, HR-1 receptor.  
 XX HR-1 receptor; cytokine receptor; peptide hormone receptor; human;  
 KW Infection; burn; trauma; asthma; allergy; AIDS; aplastic anaemia;

KW neutropaenia; therapy.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT Peptide 1..21  
 FT Protein /label= sig\_peptide  
 FT 22..380  
 FT /label= Mat\_protein  
 FT /note= "Claim 14"  
 PM EP812913-A2.  
 PD 17-DEC-1997.  
 PE 04-JUN-1997; 97EP-0303815.  
 PR 12-JUN-1996; 96US-0017843.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PA (SMIK) SMITHKLINE BEECHAM CORP.  
 PI Appelbaum ER, Hu J;  
 DR WP1: 1998-034974/04.  
 DR N-PSDB: AAV04075.  
 PT Human cytokine/peptide hormone receptor, HR-1 receptor - useful to  
 PT increase resistance to infections in individuals with trauma and/or  
 PT burns  
 PS Claim 13: Page 27-28; 34pp: English.  
 CC This protein comprises a novel human cytokine/peptide hormone  
 CC receptor, designated HR-1 receptor. The amino acid sequence  
 CC was deduced from a cDNA clone (see AAV04075) isolated from a human  
 CC testis cDNA library. It shows 27% amino acid identity and 52%  
 CC similarity with the human interleukin-5 receptor. Also claimed are  
 CC polynucleotides encoding HR-1 receptor, vector and host cells, an  
 CC agonist to the polypeptide, antibody against the polypeptide, an  
 CC antagonist that inhibits the activity of the polypeptide, a process  
 CC for diagnosing a disease, or a susceptibility to disease, related  
 CC to expression of HR-1 receptor, and a method for identifying  
 CC compounds that activate or inhibit the HR-1 receptor. HR-1  
 CC receptor protein and polynucleotides can be used for research,  
 CC biological, diagnosis and (gene) therapy applications, e.g. to  
 CC increase resistance to infections in individuals with trauma and/or  
 CC burns, and to prevent, ameliorate, treat, diagnose and/or determine  
 CC predisposition to asthma, allergic disorders or disorders of  
 CC haematopoiesis induced by AIDS, aplastic anaemia, congenital or  
 CC cyclic neutropaenia or as a consequence of cytotoxic therapy of  
 CC cancer, lymphoma, leukaemia and/or bone marrow transplantation.  
 CC  
 xx Sequence 380 AA:  
 Query Match 100.0%; Score 2104; DB 19; Length 380;  
 Best Local Similarity 100.0%; Pred. No. 2e-197;  
 Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 50  
 QY 1 MAFVCLAIGCLYTLFLISTFTGCTSSDTEIKVNPQDFEIVDPGYLYLQWQPPSLD 60  
 DB 1 MAFVCLAIGCLYTLFLISTFTGCTSSDTEIKVNPQDFEIVDPGYLYLQWQPPSLD 60  
 QY 61 HFECTVEYELKYNIGSETWTKTITTKNLHYKDGFDLKKGIKAKHTLLPMQCTNGSEVQ 120  
 DB 61 HFECTVEYELKYNIGSETWTKTITTKNLHYKDGFDLKKGIKAKHTLLPMQCTNGSEVQ 120  
 QY 121 SSMATTYTWISPOGIPETKVDMDCVYNNMQYLCSMKPGIGVLDNTYNLFWYEGIDH 180  
 DB 121 SSMATTYTWISPOGIPETKVDMDCVYNNMQYLCSMKPGIGVLDNTYNLFWYEGIDH 180  
 QY 181 ALOCVDYTKADGONIGCFPPYLEASDYKDFYICVNGSSENKPIRSSYTFPOLQNTVPLP 240  
 DB 181 ALOCVDYTKADGONIGCFPPYLEASDYKDFYICVNGSSENKPIRSSYTFPOLQNTVPLP 240

```

Db 181 ALQCVDIKADGQNGICRFPYLEASDYKDFYICVNGSSENKPIRSSYFTPOLQNIIVKPLP 240
QY 241 PVLFTFRESSCEIKLKWISIPLGPIPARCFDEIEIRDDDTTLVATVAVENETYLKKTNE 300
Db 241 PVLFTFRESSCEIKLKWISIPLGPIPARCFDEIEIRDDDTTLVATVAVENETYLKKTNE 300
QY 301 TROLCEVVRKSVNIYCSDDGIWSEMSDKQCEGEDLSKRTLLRFLPRGFILLIVIFVTG 360
Db 301 TROLCEVVRKSVNIYCSDDGIWSEMSDKQCEGEDLSKRTLLRFLPRGFILLIVIFVTG 360
QY 361 LLRRKPNTPYRKMIPEFCDT 380
Db 361 LLRRKPNTPYRKMIPEFCDT 380

RESULT 6
AAW33603 standard; Protein: 380 AA.
AAW33603:
AAW33603:
XX 08-JUN-1998 (first entry)
DT
XX Homo sapiens HR-1 receptor.
DE
XX Cytokine; hormone receptor; AIDS; acquired immune deficiency;
KW syndrome; aplastic anaemia; neutropenia; cancer treatment;
KW infection resistance; diagnosis; tumours; HR-1 receptor;
KW asthma; allergic; haematopoietic; disorder.
XX
XX Homo sapiens.
40S
XX
FH Key 1.21 location/Qualifiers
FT Peptide /note= "signal peptide"
2, XX
XX WO9747742-A1.
PN
XX 18-DEC-1997.
PD
XX
XX 09-JUL-1996; 96WO-US11459.
PF
XX 12-JUN-1996; 96WO-US10262.
PR
XX 12-JUN-1996; 96US-0017843.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA (SMIT ) SMITHKLINE BEECHAM CORP.
PI
XX Appelbaum ER, Hu J;
XX
XX WPI: 1998-052309/05.
DR N-PSDB: AAV02295.
XX
XX DNA encoding human cytokine-peptide hormone receptor - useful for
PT treating preventing or diagnosing, e.g. lowered resistance to
PT infection, asthma, allergy, or haematopoietic disease
XX
XX Claim 15; Fig 1; 75pp; English.
PS
XX The sequence is that of the human cytokine/peptide hormone receptor
CC (HR-1 receptor). This, or it's activators or agonists, can be used to
CC treat, prevent or diagnose predisposition to lowered resistance to
CC infection, asthma, allergic or haematopoietic disorders, e.g. where
CC induced by acquired immune deficiency syndrome (AIDS), aplastic anaemia,
CC neutropenia or cytotoxic treatments for cancer. Antagonists of the
CC receptor, e.g. antibodies or fragments of it may be used to treat
CC conditions associated with overexpression of the HR-1 receptor, e.g.
CC those listed above. Antibodies may also be used to assay levels of HR-1
CC receptor, overexpression of which may be diagnostic of tumours, by usual
CC immunoassays; to isolate and identify HR-1 receptor-expressing cells; or
CC for affinity purification of the HR-1 receptor.
XX
XX Sequence 380 AA;
SQ

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Query Match 100.0%; Score 2104; DB 19; Length 380;
Best Local Similarity 100.0%; Pred. No. 2e-197;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLAIGCLYTLFIISTFGCTSSSDPEIRVNPQDEIYDPGLGYLQWQPPSLD 60
Db 1 MAFVCLAIGCLYTLFIISTFGCTSSSDPEIRVNPQDEIYDPGLGYLQWQPPSLD 60
QY 61 HFKECTVEYELKRNIGSETWKTITTKNLHKDGLDKGIEAKIHTLLPQCINGSEVQ 120
Db 61 HFKECTVEYELKRNIGSETWKTITTKNLHKDGLDKGIEAKIHTLLPQCINGSEVQ 120
QY 121 SSMAETTYWISPOGIPETKVODMDCVYNNWOYLCSMKRPGIGVLLDTNYNLFYWEGLDH 180
Db 121 SSMAETTYWISPOGIPETKVODMDCVYNNWOYLCSMKRPGIGVLLDTNYNLFYWEGLDH 180
QY 181 ALQCVDIKADGQNGICRFPYLEASDYKDFYICVNGSSENKPIRSSYFTPOLQNIIVKPLP 240
Db 181 ALQCVDIKADGQNGICRFPYLEASDYKDFYICVNGSSENKPIRSSYFTPOLQNIIVKPLP 240
QY 241 PVLFTFRESSCEIKLKWISIPLGPIPARCFDEIEIRDDDTTLVATVAVENETYLKKTNE 300
Db 241 PVLFTFRESSCEIKLKWISIPLGPIPARCFDEIEIRDDDTTLVATVAVENETYLKKTNE 300
QY 301 TROLCEVVRKSVNIYCSDDGIWSEMSDKQCEGEDLSKRTLLRFLPRGFILLIVIFVTG 360
Db 301 TROLCEVVRKSVNIYCSDDGIWSEMSDKQCEGEDLSKRTLLRFLPRGFILLIVIFVTG 360
QY 361 LLRRKPNTPYRKMIPEFCDT 380
Db 361 LLRRKPNTPYRKMIPEFCDT 380

RESULT 7
AAW95296 standard; Protein: 380 AA.
AAW95296:
AAW95296:
XX 12-SEP-2000 (first entry)
DT
XX IL-13 binding chain of human IL-13 receptor.
DE
XX
XX Interleukin-13 receptor; IL-13 binding chain; IL-13bc; mouse;
KW cytokine receptor; haematopoietic receptor; atopy; allergy; asthma;
KW immune complex disease; lupus; nephritis; thyroiditis;
KW Grave's disease; inflammatory; infection; therapy; antiallergic;
KW antiinflammatory; antiasthmatic; vaccine.
XX
XX Homo sapiens.
XX
XX
FH Key 1.25 location/Qualifiers
FT Peptide /note= "signal peptide"
FT Protein 26..380
FT Domain /note= "mature protein"
FT 26..341
FT /note= "extracellular domain; a polypeptide
FT comprising amino acids 22-334 is
FT specifically claimed in Claim 11(e)"
FT
FT Domain 342..362
FT /note= "transmembrane domain"
FT 363..380
FT /note= "intracellular domain; a polypeptide
FT comprising amino acids 257-383 is
FT specifically claimed in Claim 11(f)"
XX
XX WO200036103-A1.
XX 22-JUN-2000.
XX
XX 13-DEC-1999; 99WO-US29493.
XX
XX

```

XX 14-DEC-1998; 9805-0211335.  
XX  
PR (GEM ) GENETICS INST INC.  
PA (UYJO ) UNIV JOHNS HOPKINS.  
XX  
XX Collins M, Donaldson D, Fitz L, Neben T, Whitters MJ, Wood C;  
PI Wills-Karp M;  
XX  
XX WPI: 2000-431587/37.  
DR N-PSDB: AAA27912.  
XX  
PT New polynucleotide encoding an interleukin-13 (IL-13) binding chain of  
an IL-13 receptor for treating IGE-mediated conditions, such as atopy,  
PT asthma, Grave's disease and inflammatory conditions of the lung -  
XX  
XX Claim 11(d); Page 53-54; 60pp; English.

CC The present sequence is that of the interleukin-13 binding chain  
CC (IL-13bc) of the human IL-13 receptor, as deduced from an isolated  
CC human testis cDNA clone (see AAA27912). IL-13bc is a member of  
CC the haematopoietin receptor family that acts as a mediator of  
CC IL-13. The invention provides methods for the recombinant  
CC production of IL-13bc polypeptides, including claimed full-length  
CC IL-13bc, its extracellular domain, and its intracellular domain.  
CC IL-13bc polypeptides, particularly soluble IL-13bc polypeptides,  
CC and IL-13 receptor inhibitors (e.g. antagonists of the interaction  
CC of IL-13 and its receptor) can be used to treat conditions in  
CC which IL-13 is implicated, particularly Ige-mediated conditions and  
CC diseases including atopy, allergy, asthma, immune complex diseases  
CC (e.g. lupus, nephrotic syndrome, nephritis, glomerulonephritis,  
CC thyroiditis and Grave's disease), lung inflammation,  
CC immunodeficiency, and cancer. Since IL-13 inhibits macrophage  
CC activation, IL-13bc proteins can also be used to enhance macrophage  
CC activation, e.g. in vaccination, treatment of mycobacterial or  
CC intracellular organisms or parasite infections. IL-13bc proteins  
CC may also be used to potentiate the effects of IL-13 in vitro and  
CC in vivo, as diagnostic agents, and to screen for agents capable of  
CC binding to IL-13bc or IL-13 receptor, or which interfere with the  
CC binding of IL-13 to its receptor.

XX Sequence 380 AA;

Query Match 100.0%; Score 2104; DB 21; Length 380;

Best Local Similarity 100.0%; Pred. No. 2e-197;

Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLAIIGCYLTLISTFECTSSDTEIKVNPPODFEIVDPGLYLYQWOPPLSLD 60  
D 1 MAFVCLAIIGCYLTLISTFECTSSDTEIKVNPPODFEIVDPGLYLYQWOPPLSLD 60  
D 1 HFKECTVEYELKYNIGSETWKTITITKLNHKKDGFDLNKGIEAKIHILLPQCINGSEVQ 120  
D 61 HFKECTVEYELKYNIGSETWKTITITKLNHKKDGFDLNKGIEAKIHILLPQCINGSEVQ 120  
QY 121 SSMAETTYWISPOGIPETKVODMOCVYYNMQYLLCSMKPGIGVLLDNYNLFYWEGLDH 180  
D 121 SSMAETTYWISPOGIPETKVODMOCVYYNMQYLLCSMKPGIGVLLDNYNLFYWEGLDH 180  
QY 121 SSMAETTYWISPOGIPETKVODMOCVYYNMQYLLCSMKPGIGVLLDNYNLFYWEGLDH 180  
D 121 SSMAETTYWISPOGIPETKVODMOCVYYNMQYLLCSMKPGIGVLLDNYNLFYWEGLDH 180  
QY 181 ALQCVDYIKAGQINIGCFPLEASDYKDFYICVNGSSENKPIRSSYFTFQLONIIVKPLP 240  
D 181 ALQCVDYIKAGQINIGCFPLEASDYKDFYICVNGSSENKPIRSSYFTFQLONIIVKPLP 240  
QY 241 PVLTLFTRESSCEIKLKWISPLGPIPARCFDYEIEIRDDTTLVATVENEYTLTKTTNE 300  
D 241 PVLTLFTRESSCEIKLKWISPLGPIPARCFDYEIEIRDDTTLVATVENEYTLTKTTNE 300  
QY 301 TROLCEVVRSKVNIYCSDDGIMSEMSKQCEGEGEDLSKKTLLRFLPFGFILLIVFTVG 360  
D 301 TROLCEVVRSKVNIYCSDDGIMSEMSKQCEGEGEDLSKKTLLRFLPFGFILLIVFTVG 360  
QY 361 LLRKPNTPYPMIDPEFCDT 380  
D 361 LLRKPNTPYPMIDPEFCDT 380

Db 361 LLRKPNTPYPMIDPEFCDT 380

RESULT 8

AA663812  
ID AAG63812 standard; Protein; 380 AA.

XX  
AC AAG63812;

XX 29-OCV-2001 (first entry)

XX Amino acid sequence of human interleukin-13 receptor subunit alpha 2.

XX Human; interleukin-13 receptor subunit alpha 2; IL-13Ralpha2; cancer;

XX testis antigen; immune response; glioma cell.

OS Homo sapiens.

XX WO200158479-A1.

XX 16-AUG-2001.

XX 08-FEB-2001; 2001MO-US04384.

XX 08-FEB-2000; 2000US-0181000.

XX (PENN-) PENN STATE RES FOUND.

PI Debinski W;

XX WPI: 2001-522435/57.

DR N-PSDB: AAH74791.

PT Stimulating immune response against interleukin-13 receptor alpha2

PT subunit in a subject having or at risk of developing gliomas, involves

PT formulating a vaccine comprising an agent that stimulates immune

PT response against the subunit -

PS Claim 3; Fig 1; 66pp; English.

CC The present sequence represents a human interleukin-13 receptor subunit

CC alpha 2 (IL-13Ralpha2), which is a cancer/testis antigen. The

CC specification describes a method for stimulating immune response

CC against IL-13Ralpha2 subunit. The method is used for stimulating

CC immune response against IL-13Ralpha2 in a human being having or at

CC risk of developing a cancer having glioma cells expressing IL-13Ralpha2.

CC The polypeptides and polynucleotides are useful for preventing and/or

CC treating cancers e.g., high grade gliomas (HGG).

XX Sequence 380 AA;

Query Match 100.0%; Score 2104; DB 22; Length 380;

Best Local Similarity 100.0%; Pred. No. 2e-197;

Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFVCLAIIGCYLTLISTFECTSSDTEIKVNPPODFEIVDPGLYLYQWOPPLSLD 60  
D 1 MAFVCLAIIGCYLTLISTFECTSSDTEIKVNPPODFEIVDPGLYLYQWOPPLSLD 60  
D 1 HFKECTVEYELKYNIGSETWKTITITKLNHKKDGFDLNKGIEAKIHILLPQCINGSEVQ 120  
D 61 HFKECTVEYELKYNIGSETWKTITITKLNHKKDGFDLNKGIEAKIHILLPQCINGSEVQ 120  
QY 121 SSMAETTYWISPOGIPETKVODMOCVYYNMQYLLCSMKPGIGVLLDNYNLFYWEGLDH 180  
D 121 SSMAETTYWISPOGIPETKVODMOCVYYNMQYLLCSMKPGIGVLLDNYNLFYWEGLDH 180  
QY 181 ALQCVDYIKAGQINIGCFPLEASDYKDFYICVNGSSENKPIRSSYFTFQLONIIVKPLP 240  
D 181 ALQCVDYIKAGQINIGCFPLEASDYKDFYICVNGSSENKPIRSSYFTFQLONIIVKPLP 240  
QY 241 PVLTLFTRESSCEIKLKWISPLGPIPARCFDYEIEIRDDTTLVATVENEYTLTKTTNE 300  
D 241 PVLTLFTRESSCEIKLKWISPLGPIPARCFDYEIEIRDDTTLVATVENEYTLTKTTNE 300

Db 241 PVLFTFTRESSCEIKLWMSIPGIPARCFDYEIEIREDDTTLVATVENEYTLKTTNE 300  
Qy 301 TROLCEFYVRKSVNITYGSDDDGIWSEMSDKOCWEGEDLSKKTLLRPWLPPGFTLLIVFVTG 360  
Db 301 TROLCEFYVRKSVNITYGSDDDGIWSEMSDKOCWEGEDLSKKTLLRPWLPPGFTLLIVFVTG 360  
Qy 361 LLRRKPMTYPKMIPEFCDF 380  
Db 361 LLRRKPMTYPKMIPEFCDF 380  
RESULT 9  
AAV72136  
ID AAV72136 standard; Protein; 380 AA.  
XX AAV72136;  
AC AAV72136;  
XX 24-APR-2001 (first entry)  
XX Human Interleukin (IL)-13 binding chain of IL-13 receptor (IL13bc).  
XX Human: IL-13; Interleukin-13 binding chain of IL-13 receptor; IL13bc;  
KW therapy; tissue fibrosis; Schistosoma infection; surgical incision;  
KW cytosstatic; wound; IL-13 related condition; allergic condition;  
KW nephrotic syndrome; thyroiditis; Grave's disease; cancer;  
KW macrophage activation.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
FH 1..25  
FT /label= signal\_peptide  
FT 1..81  
FT /note= "this region is identical to the translated  
FT sequence of an expressed sequence tag (EST) identified  
FT as y999f10.r1 human cDNA clone 41648 5"  
FT 26..380  
FT /label= Mature\_human\_interleukin (IL)-13\_binding\_chain\_  
FT of\_IL-13\_receptor  
FT 26..341  
FT Domain /note= "Extracellular domain; this region is specifically  
FT /note= claimed in claims 1e, 6e, 15e and 23e"  
FT 342..362  
FT Domain /note= "Transmembrane domain"  
FT 363..380  
FT /note= "intracellular domain; this region is specifically  
FT claimed in claims 1f, 6f, 15f and 23f"  
PN WO200078336-A1.  
XX 28-DEC-2000.  
PD 21-JUN-2000; 2000WO-US17103.  
PE 21-JUN-1999; 99US-0334512.  
PR 21-JUN-1999; 99US-0334512.  
XX (GEMY ) GENETICS INST INC.  
PA (UYJO ) UNIV JOHN HOPKINS.  
XX Collins M, Donaldson D, Filtz L, Neben T, Whilters MJ, Wood C;  
PI Willis-Karp M;  
XX WPI: 2001-080753/09.  
DR N-PSDB; AADD2335.  
XX Treating tissue fibrosis and/or inhibiting formation of tissue fibrosis  
PT in a mammalian subject, involves administering a pharmaceutical  
PT composition comprising IL-13 antagonist -  
XX  
PS Claim 1a: Page 69-70; 72pp; English.  
XX The invention relates to a method of treating, or inhibiting  
CC the formation of tissue fibrosis in mammals, which involves

CC administering a pharmaceutical composition comprising interleukin  
CC (IL)-13 antagonist. The protein of the invention is useful for  
CC treating tissue fibrosis resulting from infection with Schistosoma  
CC or from healing of a wound which is a surgical incision, or  
CC inhibiting formation of tissue fibrosis which affects tissues such  
CC as liver, skin epidermis and endodermis, muscle, tendon, cartilage,  
CC cardiac tissue, pancreas, lung, uterine tissue, neural tissue,  
CC testis, ovary, adrenal gland, artery, vein, colon, small intestine,  
CC biliary tract and gut. It is also used in the treatment or modulation  
CC of various IL-13 related conditions such as allergic conditions,  
CC nephrotic syndrome, thyroiditis, Grave's disease and cancer.  
CC The present sequence is human interleukin (IL)-13  
CC binding chain of IL-13 receptor (IL-13bc). IL-13bc protein is used  
CC to potentiate the effects of IL-13. This protein is also used to  
CC enhance macrophage activation and hence can be used in vaccination  
CC or treatment of mycobacterial or parasitic infections.  
XX  
XX Sequence 380 AA;  
Qy 1 MAFVCLAIGCLYPTFLISTFTGCTSSDTEIKVNPPOFEIYDPGLGYLQWQPPSLD 60  
Db 1 MAFVCLAIGCLYPTFLISTFTGCTSSDTEIKVNPPOFEIYDPGLGYLQWQPPSLD 60  
Qy 61 HFKECTVEYELKRYNIGSEFWKTIITNKLHAKDGFDLNKGIEAKIHWLLPMQCTNGSEVQ 120  
Db 61 HFKECTVEYELKRYNIGSEFWKTIITNKLHAKDGFDLNKGIEAKIHWLLPMQCTNGSEVQ 120  
Qy 121 SSWAETTYWISPOGIPETFKVODMDCVYNNQYLLCSMKPGIGVLDPNNYLFYVEGLDH 180  
Db 121 SSWAETTYWISPOGIPETFKVODMDCVYNNQYLLCSMKPGIGVLDPNNYLFYVEGLDH 180  
Qy 181 ALQGVYIKADGQNGIGRFPYLEASDYKDFYICVNGSSEKPKIRSSYFTQLOQIVAPLP 240  
Db 181 ALQGVYIKADGQNGIGRFPYLEASDYKDFYICVNGSSEKPKIRSSYFTQLOQIVAPLP 240  
Qy 241 PVLFTFTRESSCEIKLWMSIPGIPARCFDYEIEIREDDTTLVATVENEYTLKTTNE 300  
Db 241 PVLFTFTRESSCEIKLWMSIPGIPARCFDYEIEIREDDTTLVATVENEYTLKTTNE 300  
Qy 301 TROLCEFYVRKSVNITYGSDDDGIWSEMSDKOCWEGEDLSKKTLLRPWLPPGFTLLIVFVTG 360  
Db 301 TROLCEFYVRKSVNITYGSDDDGIWSEMSDKOCWEGEDLSKKTLLRPWLPPGFTLLIVFVTG 360  
Qy 361 LLRRKPMTYPKMIPEFCDF 380  
Db 361 LLRRKPMTYPKMIPEFCDF 380  
RESULT 10  
AAB29748  
ID AAB29748 standard; Protein; 380 AA.  
XX AAB29748;  
XX 23-FEB-2001 (first entry)  
DE Human IL-13 receptor IL-13 binding chain (IL-13bc).  
XX  
KW Human: IL-13 receptor; Interleukin-13; IL-13 binding chain;  
KW IL-13bc; IL-13 antagonist; fibrosis inhibition; scarring; vulnerary;  
KW wound healing; schistosoma infection; liver; skin; muscle;  
KW cartilage; cardiac tissue; lung tissue; uterine tissue;  
KW intestinal tissue; vascular tissue; neural tissue.  
XX  
OS Homo sapiens.  
XX  
PN WO200064944-A1.  
XX 02-NOV-2000.

XX 28-APR-2000: 2000MO-US11612.  
PF  
XX  
XX 28-APR-1999: 99US-0301808.  
PR  
XX  
PA (GEMT) GENETICS INST INC.  
PI Wynn TA, Chiaramonte MG, Collins M, Donaldson D, Fitz L, Neben T;  
PI Whitters MJ, Wood C;  
DR MPI: 2001-024676/03.  
DR N-PSDB: AAC81416.  
PT Treating or inhibiting tissue fibrosis resulting from infection with  
PT schistosoma and wound healing involves administering interleukin-13 or  
PT Interleukin-4 antagonist  
XX  
XX  
PS Claim 1; Page 76-77; 82pp: English.  
CC The invention relates to a method of treating fibrosis in a mammal  
CC by administering an interleukin-13 (IL-13) antagonist or an IL-4  
CC antagonist. In particular, the IL-13 antagonist is the IL-13 binding  
CC chain (IL-13bc; AAB29747, AAB29748) of the IL-13 receptor (IL-13R), or  
CC soluble fragments thereof. The method is useful for treating or  
CC inhibiting the formation of tissue fibrosis resulting from the healing  
CC of a wound, including a surgical incision wound, or from infection with  
CC schistosoma. The method may be used to treat fibrosis in a variety of  
CC tissues, particularly liver tissue, but also skin epidermis, skin  
CC endoderms, muscle, tendon, cartilage, cardiac tissue, pancreatic  
CC tissue, lung tissue, uterine tissue, neural tissue, testis, ovary,  
CC adrenal gland, artery, vein, colon, small intestine, biliary tract or gut  
CC tissue. The present sequence represents human IL-13bc.  
XX  
XX  
SQ Sequence 380 AA:  
Y  
Query Match 100.0%; Score 2104; DB 22; Length 380;  
Best Local Similarity 100.0%; Pred. No. 2e-197;  
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Y 1 MAFVCLAIIGLTYFLISTFGCTSSPTETKVNPPDFEIVDPGYLGTYLWQMPPLSLD 60  
DB 1 MAFVCLAIIGLTYFLISTFGCTSSPTETKVNPPDFEIVDPGYLGTYLWQMPPLSLD 60  
QY 61 HFKECTVEYELKYNIGSETWKTITTKNLHYKDGFDLNGIEAKIHTLPMQCTNGSEVQ 120  
DB 61 HFKECTVEYELKYNIGSETWKTITTKNLHYKDGFDLNGIEAKIHTLPMQCTNGSEVQ 120  
QY 121 SSMAETTYWISPGIPTKQDMDCVYNNQYLLCSWKPGIGVLDITNMYLFWEGLDH 180  
DB 121 SSMAETTYWISPGIPTKQDMDCVYNNQYLLCSWKPGIGVLDITNMYLFWEGLDH 180  
QY 181 ALQCVDIKADGONIGCRFPYLEASDYKADFYICVNGSSEKPKRSSFTFQLONIYVPLP 240  
DB 181 ALQCVDIKADGONIGCRFPYLEASDYKADFYICVNGSSEKPKRSSFTFQLONIYVPLP 240  
QY 241 PVLFTFRESSCEIKLWISPLGPAPCFDYEIEIRREDDTTLVATAVENEYTLTKTNE 300  
DB 241 PVLFTFRESSCEIKLWISPLGPAPCFDYEIEIRREDDTTLVATAVENEYTLTKTNE 300  
QY 301 TROLCPVNRKVNINCSDDDIWSEMSKQWEGEDLSKTLRLFRWLPFGILILIVITVG 360  
DB 301 TROLCPVNRKVNINCSDDDIWSEMSKQWEGEDLSKTLRLFRWLPFGILILIVITVG 360  
QY 361 LLLRKPTYPKMIPEFCDT 380  
DB 361 LLLRKPTYPKMIPEFCDT 380  
RESULT 11  
ID AAM49201  
XX AAM49201 standard; protein; 380 AA.  
AC AAM49201;  
--

XX 28-JUN-2002 (first entry)  
DT  
XX  
XX Human IL-13R alpha-2 chain, SEQ ID NO:1.  
DE  
XX  
XX Human; IL-13R alpha-2 chain; interleukin-13 receptor; sensitisation;  
KW IL-13 immunocjugate; immunotoxin; growth inhibition; cancer; tumour;  
KW brain; head and neck; squamous cell carcinoma; breast; liver; lung;  
KW mesothelioma; pancreatic; colon; gastric; ovarian; renal; bladder;  
KW prostate; testicular; skin; cervical; uterine; sarcoma; cytostatic;  
KW gene therapy; drug targeting; receptor.  
XX  
XX Homo sapiens.  
OS  
PN WO200217968-A2.  
PD  
XX 07-MAR-2002.  
PF  
XX 15-AUG-2001; 2001MO-US25663.  
PR 31-AUG-2000; 2000US-229842P.  
XX  
XX (US98 ) US DEPT HEALTH & HUMAN SERVICES.  
PA  
XX Puri RK;  
XX MPI: 2002-329734/36.  
XX N-PSDB: ABL55245.  
DR  
PT Use of nucleic acid or vector encoding interleukin-13 receptor alpha 2  
PT chain polypeptide that binds IL-13, for sensitizing a cancer cell e.g.  
PT brain cancer cell to effector molecule or inhibiting growth of cancer  
PT cell -  
XX  
PS Claim 1; Page -: 80pp: English.  
XX  
XX The invention relates to the use of a nucleic acid or vector  
CC encoding a polypeptide with at least 70% identity to interleukin-13  
CC receptor alpha-2 chain (IL-13R alpha-2; AAM49201) for rendering a  
CC cancer cell sensitive to IL-13R-targeted immunocjugates or for  
CC inhibiting the growth of a cancer cell. In some cancers that exhibit  
CC little or no expression of IL-13R, transfection with the IL-13R  
CC alpha-2 chain is sufficient to inhibit growth, while in  
CC other such cancers, the introduction of the IL-13R alpha-2 chain enables  
CC immunocjugates (such as immunotoxins) that comprise IL-13 to be  
CC targeted to the cancer cells. The method of the invention also results  
CC in the inhibition or death of cells in the tumour which were not  
CC directly transfected with the IL-13R alpha-2 chain. It is thought that  
CC transfection of at least some of the cells of a tumour with the IL-13R  
CC alpha-2 chain causes the secretion of a cytokine or other factor that  
CC attracts neutrophils, macrophages, or other lymphocytes to the tumour,  
CC which are then activated to kill the tumour cells. Because a nucleic acid  
CC encoding just the IL-13R alpha-2 chain is used, rather than a much larger  
CC nucleic acid encoding the multiple chains of the entire IL-13R, the  
CC transfection process is likely to be easier, and there should be a larger  
CC choice of vectors that can be used for transfection. A wide range of  
CC cancers can be treated using the methods of the invention, including  
CC brain cancer, head and neck cancer (preferably squamous cell carcinoma),  
CC breast cancer, liver cancer, lung cancer, mesothelioma, pancreatic  
CC cancer, colon cancer, gastric cancer, ovarian cancer, renal cancer,  
CC bladder cancer, prostate cancer, testicular cancer, skin cancer, cervical  
CC cancer, uterine cancer, or sarcoma. The present sequence represents  
CC the human IL-13R alpha-2 chain which is specifically claimed for  
CC use in the method of the invention.  
CC Note: The present sequence is not shown in the specification, but was  
CC obtained from Genbank using the accession number (X95302) referred to on  
CC page 13.  
XX  
XX  
SQ Sequence 380 AA:  
Y  
Query Match 100.0%; Score 2104; DB 23; Length 380;  
Best Local Similarity 100.0%; Pred. No. 2e-197;  
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



QY 1 MAFVCLAIGCLYTFLLISTTFCGTSSSDTEIKVNPQDPEIYDPCYLGTYLQWQPPSLD 60  
 DB 1 MAFVCLAIGCLYTFLLISTTFCGTSSSDTEIKVNPQDPEIYDPCYLGTYLQWQPPSLD 60  
 QY 61 HFKECTVEYELKYNIGSETWKTITTKNLHYKDGFDLNKGIEAKIHLLPQCCTNGSEVQ 120  
 DB 61 HFKECTVEYELKYNIGSETWKTITTKNLHYKDGFDLNKGIEAKIHLLPQCCTNGSEVQ 120  
 QY 121 SSMAETTYWISPOGIPETKVQDMDCVYYNMQYLLCSMKPGIGVLLDTNYNLFWYEGLDH 180  
 DB 121 SSMAETTYWISPOGIPETKVQDMDCVYYNMQYLLCSMKPGIGVLLDTNYNLFWYEGLDH 180  
 QY 181 ALQCVDIKADGONIGCFRPLEASDYKDFYICVNGSSENNPIRSSYTFPOLQNVKPLP 240  
 DB 181 ALQCVDIKADGONIGCFRPLEASDYKDFYICVNGSSENNPIRSSYTFPOLQNVKPLP 240  
 241 PVLFTFTRESSCEIKLWKSIPLGPIPARCFDYEIEIRDDTTLVATVENEFTYTLKTNE 300  
 241 PVLFTFTRESSCEIKLWKSIPLGPIPARCFDYEIEIRDDTTLVATVENEFTYTLKTNE 300  
 QY 301 TROLCFVVRKVNITYCSDGIMSEMSDKQCEGEBLSKKTLLRFLPFGFILLIVIEVTG 360  
 DB 301 TROLCFVVRKVNITYCSDGIMSEMSDKQCEGEBLSKKTLLRFLPFGFILLIVIEVTG 360  
 QY 361 LLRKPNTPYPMIPEFCDT 380  
 DB 361 LLRKPNTPYPMIPEFCDT 380

RESULT 12  
 AAW36614  
 ID AAW36614 standard; Protein: 380 AA.  
 AC AAW36614;  
 XX 30-MAR-1998 (first entry)  
 DE Human zcytor2 cytokine receptor protein.  
 KW Cytokine receptor; ligand binding; testicular cell; spermatogenesis;  
 OS Homo sapiens.  
 XX W09733913-A1.  
 18-SEP-1997.  
 PF 12-MAR-1997; 97WO-US04043.  
 PR 13-MAR-1996; 96US-0013345.  
 PA (ZYMO ) ZYMOGENETICS INC.  
 PI Baumgartner JW, Farrah TM, Foster DC, Grant FJ;  
 PI O'Hara PJ;  
 DR WPI; 1997-4/0820/43.  
 DR N-PSDB; AAT96783.  
 XX New nucleic acid encoding testis-specific cytokine receptor - useful  
 PT for identification of ligands or antagonists, potentially for use as  
 PT male contraceptives or for infertility treatment  
 PS Claim 1; Page 51-53; 79pp; English.  
 XX This sequence represents a novel ligand-binding receptor, zcytor2, which  
 CC shares homology with cytokine receptors and was isolated from a human  
 CC testis cDNA library. The resulting polypeptide is a receptor for  
 CC cytokines (particularly interleukin-13) and is expressed on the surface  
 CC of testicular cells, probably being involved in spermatogenesis. It can  
 CC be used to detect ligands that promote proliferation and/or

CC differentiation of such cells in cultures and may also be used to treat  
 CC infertility. Antagonists of this receptor may be used to characterise  
 CC ligand-receptor interactions and as male-specific contraceptives. By  
 CC blocking the action of IL-13, receptor antagonists and ligand-binding  
 CC this receptor can also be used to modulate immune function, e.g. in  
 CC allergy and asthma, as a diagnostic to determine circulating levels of  
 CC ligand and also to isolate and purify ligands. Antibodies can be used to  
 CC assay circulating receptor (an abnormal level may be indicative of  
 CC disease such as cancer), for labelling cells that express the receptor,  
 CC and therapeutically as antagonist.  
 XX Sequence 380 AA;  
 SQ  
 Query Match 98.8%; Score 2078; DB 18; Length 380;  
 Best Local Similarity 99.2%; Pred. No. 6.9e-195;  
 Matches 377; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 MAFVCLAIGCLYTFLLISTTFCGTSSSDTEIKVNPQDPEIYDPCYLGTYLQWQPPSLD 60  
 DB 1 MAFVCLAIGCLYTFLLISTTFCGTSSSDTEIKVNPQDPEIYDPCYLGTYLQWQPPSLD 60  
 QY 61 HFKECTVEYELKYNIGSETWKTITTKNLHYKDGFDLNKGIEAKIHLLPQCCTNGSEVQ 120  
 DB 61 HFKECTVEYELKYNIGSETWKTITTKNLHYKDGFDLNKGIEAKIHLLPQCCTNGSEVQ 120  
 QY 121 SSMAETTYWISPOGIPETKVQDMDCVYYNMQYLLCSMKPGIGVLLDTNYNLFWYEGLDH 180  
 DB 121 SSMAETTYWISPOGIPETKVQDMDCVYYNMQYLLCSMKPGIGVLLDTNYNLFWYEGLDH 180  
 QY 181 ALQCVDIKADGONIGCFRPLEASDYKDFYICVNGSSENNPIRSSYTFPOLQNVKPLP 240  
 DB 181 ALQCVDIKADGONIGCFRPLEASDYKDFYICVNGSSENNPIRSSYTFPOLQNVKPLP 240  
 QY 241 PVLFTFTRESSCEIKLWKSIPLGPIPARCFDYEIEIRDDTTLVATVENEFTYTLKTNE 300  
 DB 241 PVLFTFTRESSCEIKLWKSIPLGPIPARCFDYEIEIRDDTTLVATVENEFTYTLKTNE 300  
 QY 301 TROLCFVVRKVNITYCSDGIMSEMSDKQCEGEBLSKKTLLRFLPFGFILLIVIEVTG 360  
 DB 301 TROLCFVVRKVNITYCSDGIMSEMSDKQCEGEBLSKKTLLRFLPFGFILLIVIEVTG 360  
 QY 361 LLRKPNTPYPMIPEFCDT 380  
 DB 361 LLRKPNTPYPMIPEFCDT 380

RESULT 13  
 AAW36616  
 ID AAW36616 standard; Protein: 372 AA.  
 AC AAW36616;  
 XX 30-MAR-1998 (first entry)  
 DE Celebus macaque zcytor2 protein.  
 KW Cytokine receptor; ligand binding; testicular cell; spermatogenesis;  
 OS Macaque sp.  
 XX Key location/Qualifiers  
 FT Protein 1..372  
 FT /label= zcytor2  
 FT /note= "partial protein sequence"  
 XX W09733913-A1.  
 18-SEP-1997.  
 PF 12-MAR-1997; 97WO-US04043.  
 PR 13-MAR-1996; 96US-0013345.

XX (ZYMO ) ZYMOGENETICS INC.  
PA Baumgartner JW, Farrah TM, Foster DC, Grant FJ;  
XX O'Hara PJ;  
PI WPI: 1997-470820/43.  
XX N-PSDB; AAT96784.  
DR  
XX New nucleic acid encoding testis-specific cytokine receptor - useful  
PT for identification of ligands or antagonists, potentially for use as  
PT male contraceptives or for infertility treatment  
XX  
XX Example 4; Page 56-57; 79pp; English.  
XX This sequence represents a novel ligand-binding receptor, Zcytor2,  
CC which shares homology with cytokine receptors and is isolated from  
CC testis tissue obtained from a Celebus macaque. The resulting polypeptide  
CC is a receptor for cytokines (particularly interleukin-13) and is  
CC expressed on the surface of testicular cells, probably being involved in  
CC spermatogenesis. It can be used to detect ligands promoting proliferation  
CC and/or differentiation of such cells in cultures and may also be used to  
CC treat infertility. Antagonists of this receptor may be used to  
CC characterise ligand-receptor interactions and as male-specific  
CC contraceptives. By blocking the action of IL-13, receptor antagonists and  
CC ligand-binding this receptor can also be used to modulate immune  
CC function, e.g. in allergy and asthma, as a diagnostic to determine  
CC circulating levels of ligand and also to isolate and purify ligands.  
CC Antibodies can be used to assay circulating receptor (an abnormal level  
CC may be indicative of disease such as cancer), for labelling cells that  
CC express the receptor, and therapeutically as antagonist.  
XX  
SQ Sequence 372 AA;  
  
Query Match 88.1%; Score 1853; DB 18; Length 372;  
Best Local Similarity 92.2%; Pred. No. 7,4e-173;  
Matches 34; Conservative 7; Mismatches 22; Indels 0; Gaps 0;  
  
QY 1 MAFVCLAIGCLYTLPTFTGCTSSDTEIKVNPQDFEIVDPGYLYLQWOPPLSLD 60  
D 1 MAFVLAIRCLCTFLISTFTGCTSTDEIKVNPQDFEIVDPGYLYLQWOPPLSLD 60  
QY 61 HFRCCTVEYLKYNIGSEMTKTIITKMLHYKDGFDLNGKIEAKIHTLLPWOCTNGSEVQ 120  
D 61 NFKECTVEYLKYNIGSEMTKTIITKMLHYKDGFDLNGKIEAKIHTLLPWOCTNGSEVQ 120  
QY 121 SSMAETTYWISPGIPEKTVQDMDCVYNNQYLLCSWKPICIGVLDITNVLFWYEGIDH 180  
D 121 SSMAEATYWISPGIPEKTVQDMDCVYNNQYLLCSWKPICIGVLDITNVLFWYEGIDR 180  
QY 181 ALOCVDYIKADGONICRFPYLEASDKDFITCVNGSSENNKPIRSSYFTFOLQNIKPLP 240  
D 181 ALOCVDYIKADGONICRFPYLEASDKDFITCVNGSSENNKPIRSSYFTFOLQNIKPLP 240  
QY 241 PVLTLTFRESCECEIKLWMSIPLGPIPARCFYEIEIRDDTTLTATVENVETYLKLTNE 300  
D 241 PVLCTFQIESLEYELKLMWSIPLGPIPARCFYEIEIRDDTTLTATVENVETYLKLTNE 300  
QY 301 TROLCFVVRSKVNITCSDDGIMSEMSDKOCWEGEDLSKKTLLRFMLPFGFLLIVIEVTG 360  
D 301 TROLCFVVRSKVNITCSDDGIMSEMSDKOCWEGEDLSKKTLLRFMLPFGFLLIVIEVTG 360  
QY 361 LLLRKPNTYPRM 372  
D 361 LLLCRKDSYPRM 372

DT 26-FEB-2002 (first entry)  
XX Human soluble cytokine IL-13 receptor alpha2 (IL-13RA2) protein.  
DE Human soluble cytokine IL-13 receptor alpha2 (IL-13RA2) protein.  
XX  
KW Human: zalphai1: cytokine receptor; immunosuppressive; cytostatic;  
KW inflammatory disorder; haemostatic; cell proliferation; immune disorder;  
KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer;  
KW myasthenia gravis; systemic lupus erythematosus; SLE; diabetes; asthma;  
KW ulcerative colitis; inflammatory bowel disease; Crohn's disease; sepsis;  
KW viral infection; IL-13 receptor alpha2; IL-13RA2.  
XX  
OS Homo sapiens.  
XX  
XX WO200177171-A2.  
XX  
XX 18-OCT-2001.  
XX  
XX 03-APR-2001; 2001WO-US10872.  
XX  
XX 05-APR-2000; 2000US-194731P.  
XX 28-JUL-2000; 2000US-222121P.  
XX  
XX (ZYMO ) ZYMOGENETICS INC.  
XX  
XX Sprecher CA, Novak JE, West JW, Presnell SR, Holly RD, Nelson AJ;  
XX WPI: 2002-025898/03.  
XX N-PSDB; AAD22980.  
XX  
XX Novel soluble receptor polypeptides and polynucleotides used as  
PT cytokine antagonist for stimulating ligand activity-induced  
PT proliferation of hematopoietic cells and for suppressing immune  
PT response in a mammal  
XX  
XX  
XX Disclosure; Page 240-241; 243pp; English.  
XX  
XX The invention relates to an isolated soluble zalphai1 cytokine receptor  
CC polypeptide and their cDNA molecules. Zalpha proteins are useful for  
CC inhibiting or antagonising the ligand activity-induced proliferation of  
CC haematopoietic cells and haematopoietic cell progenitors preferably  
CC lymphoid cells which are natural killer cells or cytotoxic T cells.  
CC Zalpha is useful for treating immune and inflammatory disorders, for  
CC reducing proliferation of neoplastic B or T cells, for suppressing an  
CC immune response in a mammal exposed to an antigen or pathogen. Zalpha is  
CC useful for treating diseases that require immune regulation including  
CC autoimmune diseases such as rheumatoid arthritis, multiple sclerosis,  
CC myasthenia gravis, systemic lupus erythematosus (SLE) and diabetes;  
CC asthma, ulcerative colitis, inflammatory bowel disease, Crohn's disease,  
CC sepsis, viral infection (dengue virus infection) and cancer. The present  
CC sequence is human soluble cytokine IL-13 receptor alpha2 (IL-13RA2)  
CC protein related to the invention.  
XX  
SQ Sequence 317 AA;  
  
Query Match 83.8%; Score 1764; DB 23; Length 317;  
Best Local Similarity 100.0%; Pred. No. 3.1e-164;  
Matches 317; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 27 DTEIKVNPQDFEIVDPGYLYLQWOPPLSLDHFRCCTVEYLKYNIGSEMTKTIIT 86  
D 1 DTEIKVNPQDFEIVDPGYLYLQWOPPLSLDHFRCCTVEYLKYNIGSEMTKTIIT 60  
QY 87 KNLHYKDGFDLNGKIEAKIHTLLPWOCTNGSEVOSSMAETTYWISPGIPEKTVQDMDCV 146  
D 61 KNLHYKDGFDLNGKIEAKIHTLLPWOCTNGSEVOSSMAETTYWISPGIPEKTVQDMDCV 120  
QY 147 YNNQYLLCSWKPICIGVLDITNVLFWYEGIDHALDCVDYIKADGONICRFPYLEASD 206  
D 121 YNNQYLLCSWKPICIGVLDITNVLFWYEGIDHALDCVDYIKADGONICRFPYLEASD 180  
QY 207 YKDFYICVNGSSENNKPIRSSYFTFOLQNIKPLPVPVLTFTRESSCEIKLWMSIPLGPI 266  
D 181 YKDFYICVNGSSENNKPIRSSYFTFOLQNIKPLPVPVLTFTRESSCEIKLWMSIPLGPI 240

QY 267 ARCPDYIEIREDDTTLVTATVENETYYTLKTTNETRQLCFVVRSKVNIYCSDDGIWSEMS 326  
 DB 241 ARCPDYIEIREDDTTLVTATVENETYYTLKTTNETRQLCFVVRSKVNIYCSDDGIWSEMS 300  
 QY 327 DKOCWEGEDLSKKTLLR 343  
 DB 301 DKOCWEGEDLSKKTLLR 317

RESULT 15  
 ID AAM56261 standard; Protein: 315 AA.  
 AC AAM56261;  
 DT 16-SEP-1998 (first entry)

Mature interleukin-13 binding protein.

KM Therapeutic; IL-13 mediated condition; allergy; asthma; diagnosis;  
 KM autoimmune disease; antibody; immunotherapy.

OS Homo sapiens.

PN WO9810638-A1.

PD 19-MAR-1998.

PF 10-SEP-1997; 97WO-AU00591.

PR 27-FEB-1997; 97AU-0005374.

PR 10-SEP-1996; 96AU-0002262.

XX (AMRA-) AMRAD OPERATIONS PTY LTD.

XX Hilton DJ, Nicola NA, Simpson RJ, Zhang J;

XX WPI: 1998-207062/18.

DR N-PDDB; AAV22702.

XX New isolated interleukin-13 binding protein - used to develop

PT products for therapy e.g. for allergic conditions such as asthma or

PT for diagnosis or detection

XX Disclosure; Page 55-56; 69pp; English.

CC The IL-13 binding protein and related therapeutic molecules can be used  
 CC in the antagonism of at least one IL-13 activity. They can be used for  
 CC treating IL-13 mediated conditions such as certain allergic conditions  
 CC such as asthma or to inactivate locally administered IL-13 after IL-13  
 CC treatment. The products can also be used as diagnostic agents, e.g. for  
 CC detecting autoimmune diseases. The antibodies can also be used for  
 CC immunotherapy and may also be used as a diagnostic tool.

XX Sequence 315 AA;

Query Match 83.3%; Score 1753; DB 19; Length 315;

Best Local Similarity 100.0%; Pred. No. 3.7e-163; Indels 0; Gaps 0;

Matches 315; Conservative 0; Mismatches 0;

QY 29 EIKVNPPODEIYDPGILGYLYLWOPPLSLDHFKECTVEYELKYRNIGSETWTKTITKN 88  
 DB 1 EIKVNPPODEIYDPGILGYLYLWOPPLSLDHFKECTVEYELKYRNIGSETWTKTITKN 60  
 QY 89 LHYKDGFDLKKGIKIAKIHITLLPMQCTNGSEVOSSMAETTYWISPGIPEKRVQDMDCVY 148  
 DB 61 LHYKDGFDLKKGIKIAKIHITLLPMQCTNGSEVOSSMAETTYWISPGIPEKRVQDMDCVY 120  
 QY 149 NMQYLLCSMKRPGIGVLDITNINLFYWEGLDHALQCVDIKADGQNTGCRPPYLEASDYK 208  
 DB 121 NMQYLLCSMKRPGIGVLDITNINLFYWEGLDHALQCVDIKADGQNTGCRPPYLEASDYK 180

QY 209 DFYICVNGSSSEKPIRSSYFTFOLQNIYKPLPPVYLFTFTRESSCEIKLKWISIPGLPIPAR 268  
 DB 181 DFYICVNGSSSEKPIRSSYFTFOLQNIYKPLPPVYLFTFTRESSCEIKLKWISIPGLPIPAR 240  
 QY 269 CFDEYIEIREDDTTLVTATVENETYYTLKTTNETRQLCFVVRSKVNIYCSDDGIWSEMSDK 328  
 DB 241 CFDEYIEIREDDTTLVTATVENETYYTLKTTNETRQLCFVVRSKVNIYCSDDGIWSEMSDK 300  
 QY 329 QCWEGEDLSKKTLLR 343  
 DB 301 QCWEGEDLSKKTLLR 315

Search completed: January 24, 2003, 19:35:35  
 Job time : 38 secs

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OM protein - protein search, using sw model

Run on: January 24, 2003, 19:33:14 ; Search time 35 Seconds  
(without alignments)  
2237.083 Million cell updates/sec

Title: US-09-714-792a-4  
Perfect score: 2104  
Sequence: 1 MAFVCLAIICLYTFLISTF.....LLLRKPNTYPKMIPFPCDT 380

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_21:\*  
1: sp.\_archaea:\*  
2: sp.\_bacteria:\*  
3: sp.\_fungi:\*  
4: sp.\_human:\*  
5: sp.\_invertebrate:\*  
6: sp.\_mammal:\*  
7: sp.\_mhc:\*  
8: sp.\_organelle:\*  
9: sp.\_phage:\*  
10: sp.\_plant:\*  
11: sp.\_rodent:\*  
12: sp.\_virus:\*  
13: sp.\_vertebrate:\*  
14: sp.\_unclassified:\*  
15: sp.\_virus:\*  
16: sp.\_bacteriaph:\*  
17: sp.\_archaeop:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1503	71.4	386	6	Q95LFO
2	1194.5	56.8	383	11	O88786
3	1172.5	55.7	385	11	O8VHK6
4	579	27.5	404	13	O90XP8
5	311.5	14.8	420	4	O14633
6	310.5	14.8	396	4	O14631
7	302.5	14.4	405	6	O95LFI
8	298.5	14.2	415	11	O92OK4
9	297	14.1	427	4	O96BBA
10	296	14.1	426	11	O8VHC2
11	292	13.9	333	4	O15469
12	268	12.7	414	11	O92DB8
13	264.5	12.6	349	6	O97597
14	259	12.3	414	11	O99PS3
15	241.5	11.5	279	4	O9UDY5
16	240.5	11.4	249	4	O8MX09

17	222	10.6	368	6	O8S071	O8S071 sus scrofa
18	212.5	10.1	278	11	O8VHR8	O8VHR8 rattus norv
19	187	8.9	611	13	O9IBF6	O9IBF6 xenopus lae
20	187	8.9	611	13	O9PT10	O9PT10 xenopus lae
21	185.5	8.8	343	13	O9DE01	O9DE01 oncorhynch
22	178	8.5	896	11	O64146	O64146 rattus norv
23	175.5	8.3	896	11	O802X9	O802X9 mus musculu
24	174.5	8.3	611	13	O9PTM9	O9PTM9 xenopus lae
25	173.5	8.2	881	13	O57519	O57519 xenopus lae
26	170	8.1	890	11	O9Z1A0	O9Z1A0 cavia porce
27	167	7.9	622	6	O9N0J7	O9N0J7 callithrix
28	164	7.8	227	6	O9GLM3	O9GLM3 ursus marit
29	159	7.6	608	11	O99JZ1	O99JZ1 mus musculu
30	156	7.4	625	6	O9XS92	O9XS92 trichosurus
31	155	7.4	626	13	O90MG7	O90MG7 cynops pyrr
32	153.5	7.3	918	13	O9W6U9	O9W6U9 gallus gall
33	153	7.3	217	6	O46386	O46386 mustela vis
34	151	7.2	206	4	O16354	O16354 homo sapien
35	151	7.2	268	4	O8TD78	O8TD78 homo sapien
36	151	7.2	288	4	O96P36	O96P36 homo sapien
37	151	7.2	349	4	O9UHJ5	O9UHJ5 homo sapien
38	151	7.2	376	4	O96P35	O96P35 homo sapien
39	147.5	7.0	538	13	O9DFU0	O9DFU0 sparus aura
40	146.5	7.0	422	4	O9UHH5	O9UHH5 homo sapien
41	145.5	6.9	422	4	O75462	O75462 homo sapien
42	143.5	6.8	425	11	O9JMS8	O9JMS8 mus musculu
43	138	6.6	390	4	O9UEH7	O9UEH7 homo sapien
44	135	6.4	346	13	O93404	O93404 oreochromis
45	131	6.2	861	6	O9BEG2	O9BEG2 bos taurus

#### ALIGNMENTS

RESULT 1	
Q95LFO	PRELIMINARY; PRT; 386 AA.
ID Q95LFO	
AC Q95LFO	
DT 01-DEC-2001 (TREMBLrel. 19, Created)	
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)	
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)	
DE Interleukin 13 receptor alpha chain 2.	
GN IL13RA2.	
GN IL13RA2.	
OS Canis familiaris (Dog).	
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.	
OX NCBI_Taxid=9615;	
RN [1]	
RP SEQUENCE FROM N.A.	
RX MEDLINE=21287533; PubMed=11389954;	
RA Tang L.;	
RT "Molecular cloning of canine IL-13 receptor alpha chain (alpha1 and alpha2) cDNAs and detection of corresponding mRNAs in canine tissues.";	
RT tissues.";	
RL Vet. Immunol. Immunopathol. 79:181-195(2001).	
DR EMBL: AF314533; AAL14887.1; -.	
DR InterPro: IPR002996; CRIA.	
DR InterPro: IPR003532; Hemtopoptn_S_F2.	
DR POSITE; PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.	
KW Receptor.	
SO SEQUENCE	
Query Match	386 AA; 45110 MW; A16PDEF2DD023ED95 CRC64;
Best Local Similarity	71.4%; Score 1503; DB 6; Length 386;
Matches 272; Conservative 42; Mismatches 57; Indels 2; Gaps 2;	

QY	1	MAFVCLAIICLYTFLISTFGCTSSDPTETKVNRPDPETVDPGLYLVQMPPLSLD	60
DB	1	MAFLHLDVGLYTLVLTAFG-SMLSNAEIKVNPDPDEFIVDPGLYLSLQWQPPLEPD	59
QY	61	HFKECTVEYELKYNIGSETWTKTTITKNLHYKDGFDLNGKIEAKITHTLLPMOCNGSEVQ	120
DB	60	NFKECTIEYELKYNIDSEMKTKITITKNLHYKDGFDLNGKIEAKITHTLLPMOCNGSEVQ	119

QY	121	SSMETHYTWISPOCIPERKQVODMCCVYYNNQYLLCSMKPGIGVLTDPNTNVLFWYWGSDH	180
Db	120	SSMETHYTWISPOGNRETKIODMCCVYYNNQYLLCSMKPGHGHGFEDNIOLEFWYWGSDH	179
QY	181	ALOCVDYIKADQNIIGCRFPYLEASDYKDFYICVNGSSSENKPIRSSYFTQLONIYKPLP	240
Db	180	SAECTDYIKVNGKNNGCRFPLESDYKDFYICVNGSSSQPIRPSYFIQLONIYKPM	239
QY	241	PVYLTFFRESCEIKLWMSIPDGIPARCDEYEIENEDDTLLVTAVERNETHLKTNE	300
Db	240	PDIYSLTVAKNSEENLNMWMPKGPPIKPCFYLEIETFEEDGTWVTTVAENEIOITRISNE	299
QY	301	TROLCFVVRSKVNITGSDDGIMWSMSDQOCQEGEDLSKTLTLRFWTLFGFILLVLIVFTG	360
Db	300	SQIKLCFLVRSKVNITGSDDGIMWSMSDQOCWK-DIKKELTVLFFLLIPFVAVSLFVLVITC	358
QY	361	LLAKKPNTYKPMI 373	
Db	359	LLLYKORALEKTI 371	

Accession ID	Release Date	Project Name	Version
OC88786	2008-07-26	PRELIMINARY	383 AA
AC	088786		
DT	01-NOV-1998	(TrEMBLrel. 08, Created)	
DT	01-NOV-1998	(TrEMBLrel. 08, Last sequence update)	
DT	01-MAR-2002	(TrEMBLrel. 20, Last annotation update)	
DE	IL-13 receptor alpha 2 (interleukin 13 receptor, alpha 2).		
GN	IL13RA2.		
OS	Mus musculus (mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C3H/HEJ; TISSUE=THYMUS;		
RA	MEDLINE=98391042; Pubmed=9725226;		
RA	Donaldson D.D., Whitters M.J., Fitz L., Neben T.Y., Finnerty H.,		
RA	Henderson S.L., O'Hara R.M. Jr., Beler D.R., Turner K.J., Wood C.R.,		
RA	Collins M.		
RT	"The murine IL-13 receptor alpha 2: molecular cloning,		
RT	characterization, and comparison with murine IL-13 receptor alpha 1."		
IL	J. Immunol. 161:2317-2324(1998).		

RA Strausberg R.;  
 RI Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases  
 RI EMBL; U65747; AAC33240.1; "-"  
 RI EMBL; BC003723; AAH003723.1; "-"  
 DR HSSP: P16471; 1BP3.  
 DR MGD: MGI:1277954; 1113ra2.  
 DR InterPro: IPR002996; CRA.  
 DR InterPro: IPR003532; Hemopophyl\_S\_F2.  
 DR ProSite: PS01336; HEMATOPOY\_REC\_S\_F2; UNKNOWN\_1.  
 KW Receptor.  
 SQ SEQUENCE 383 AA: 44482 MW: C25212325C47E358 CRC64;

Query Match	56.8%	Score 1194.5	DB 11	Length 383
Best Local Similarly	58.9%	Pred. No. 5.3e-95		
Matches 219	Conservative 55	Mismatches 91	Indels 7	Gaps 3

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QY 1 MAFVAGCAYTFLITSTFECSTSSDTEKYNVPPOEFLVNDGAGYLQKOPPLSD 60
    |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 1 MAFV--HRCRCFLFLCTITGYS----LEKYNVPQDFELDPGLGAGYLQKMPVAV 54
    |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 61 HFKECTVEYELKYNNGISEETKTLITRNKLNHYKGFDLNKGIEAKIHTLPLQOCTNGSEVQ 120
    |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 55 KFKCCTLEYELKYNVDSDSKKTLITRNLLYKOSFDLNKGIECKIRHLSHCRTNGSEVQ 114
    |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
QY 121 SSMAETTYWISPGCIPETKYODMDCVYYNNQOYLCSMKPGIGVLLDTNVLFWYEGCLDH 180
    |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::

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Db	115	SPMIEASVIGISDEGSLFETKIDMKCIYYNMQILVCSMKPGKTVYSDNINYMFEYBGLDH	1744
Qy	181	ALOCVDYIKADGONIGCFPLELSDYKDFICYVNGSSENKPIRSSFTLOLNIYVPLP	2404
Db	175	ALOCADYIQHHEKKNVCGCLSNLSDSDYKDFEICYVNGSSKLEPISSYTVLOLNIYVPLP	2344
Qy	241	PVYLTFRESCEIKLWKSIPGLPIPRCFYEIETREDPTLTAVARENETYTLKTTNE	3004
Db	235	PEFLHISVENSIDIRMKSTGGGIIIPRCYTYETVIEDDISWESATDKMDKLKRANE	2944
Qy	301	TROLCEVVRKSVNIYCSDDGIWSEMSDQKCEGEGEDLSKTLRLFWLPGFLLILVIFVTG	3604
Db	295	SEDCELFVRKSVNIYCADDGIMSESEBCEGEGYTGDPDSKIT-FIVPCLFELFILLLLC	3534
Qy	361	LLLRKPNTYPRKM	372
Db	354	LIVERKEDEPEPTL	365

RESULT 3			
ID	Q8VHK6	PRELIMINARY;	PRT; 385 AA.
AC	Q8VHK6;		
DT	01-MAR-2002 (TrEMBLrel. 20, Created)		
DT	01-MAR-2002 (TrEMBLrel. 20, last sequence update)		
DT	01-JUN-2002 (TrEMBLrel. 21, last annotation update)		
DE	Interleukin 13 receptor alpha chain 2.		
GN	IL13RA2.		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCBI_TaxID=10116;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=SPRAGUE-DAWLEY;		
RA	Wu A.; Low W.C.;		
RT	"Molecular cloning of rat interleukin 13 receptor alpha 2 gene and its		
RT	expression in rat tissues."		
RL	Submitted (NOV-2001) to the EMBL/Genbank/DBJ databases.		
DR	EMBL; AF448818; AAL57513.1; -		
DR	InterPro: IPR002996; CRIA.		
DR	InterPro: IPR003537; Hemopoetin_S_F2.		
DR	PROSITE; PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.		
KW	RECEPTOR.		
QO	SEQUENCE 385 AA; 44622 MW; E060F0E434737E2 CRC64;		

Query Match	55.7%	Score 1172.5	-DB 11	Length 385
Best Local Similarity	56.7%	Pred. No. 4.2e-93		
Matches 211	Conservative 61	Mismatches 95	Indels 5	Gaps 2

[illegible]

QY 361 LLLKRPNTYPRK 372  
 Db 356 LIVEKEDPEPTL 367

RESULT 4  
 ID Q90XP8 PRELIMINARY; PRT; 404 AA.  
 AC Q90XP8;  
 DT 01-DEC-2001 (TREMblrel. 19, Created)  
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)  
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)  
 DE Interleukin 13 receptor alpha-2.  
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;  
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
 NCBI\_TaxID=8022;

[1]  
 SEQUENCE FROM N.A.  
 Lockyer A.E., Jones C.S., Noble L.R., Verspoor E., Holland J.,  
 RA Secombes C.J.,  
 RT "Isolation and characterization of a putative interleukin 13 receptor  
 alpha-2 sequence from rainbow trout (Oncorhynchus mykiss).";  
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF61437; AAL26927.1; -  
 DR InterPro: IPR002996; CRIA.  
 KW Receptor.  
 SQ SEQUENCE 404 AA; 46728 MW; 4B9B7E3F4CFEBD6 CRC64;

Query Match 27.5%; Score 579; DB 13; Length 404;  
 Best Local Similarity 33.8%; Pred. No. 7, 6e-42;  
 Matches 120; Conservative 74; Mismatches 143; Indels 18; Gaps 7;

QY 15 LISTFECTSSDTEIKVNPPODFEIVDPGYLYLQWOPPLSLDHFEKCTVEYELEKYR 74  
 Db 15 LLSWMSQICISQ-EFTVDPENIGIDDPCHLGPLYIHTAPASLTNLTCASMRHYLEYF 72  
 QY 75 NISGETKTIITKTLKHKDGFNLKGIKAKHTLLPWCCTNGSGVSSMAETTYWISPOG 134  
 Db 73 NTYOSRNTVTRVTWTRRAGDEKEVRVRLSTLLGACTNGTGLKSPFTEMLPPNNTG 132  
 QY 135 IPEKTVDMDCVYYNMQYLLCSMKRGIGVLDTNYNLFWEYEGDHALQCVYIKADGON 194  
 Db 133 PVGRVQGFQCVYQKRFMECTWETGLEPQSGYSLTFMHRHQAEPCQYIHSNGVR 192  
 QY 195 IGCRRPYLEASDYKDFYICVNGSSENKPIRSSYTFQLQNIKVP-LPPVYLTFTRESSC 252  
 Db 193 TGCFTFESISEFSDFNICINSSSPFVLAIRSAFSLQIQNVKPAIETVLEASPR-- 250  
 QY 253 EIKLKWSIPRLGPARGEDYEIEIREDDT--TLVTATVENE-TYTLKTNETQQLCFVY 308  
 Db 251 RLOVQWMLPRNRPRLHCLLEYEARREGVGQPLLRNVNEMTLTSLSDMGARRKCFRV 310  
 QY 309 RSKVNIYCSDDGSIWSEMSDKQCEGDELKSKTLRFMLPFGFILLIVFYTGILL 363  
 Db 311 RSRNHHCACRGRFWSMDSHMSC--HSDTESDAVY-----GCANVIGIITYSMLIL 357

RESULT 5  
 ID Q14633 PRELIMINARY; PRT; 420 AA.  
 AC Q14633;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)  
 DE Interleukin-5 receptor precursor.  
 GN HSILSR.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NCBI\_TaxID=9606;

RN [1]  
 RC SEQUENCE FROM N.A.  
 RC TISSUE-PERIPHERAL BLOOD;  
 RX MEDLINE=92121815; PubMed=1732409;  
 RA Murata Y., Takaki S., Migita M., Kikuchi Y., Tomioka A., Takatsu K.;  
 RT "Molecular cloning and expression of the human Interleukin 5  
 receptor.";  
 RL J. Exp. Med. 175:341-351(1992).  
 DR EMBL: X61176; CAA43483.1; -  
 DR InterPro: IPR002996; CRIA.  
 DR InterPro: IPR003532; Hemitoptn\_S\_F2.  
 DR PROSITE: PS01356; HEMATOPO\_REC\_S\_F2; UNKNOWN\_1.  
 KW Receptor; Signal.  
 FT SIGNAL 1 20  
 FT CHAIN 21 420  
 SQ SEQUENCE 420 AA; 47670 MW; 8DC56DFC8BEFF524 CRC64;

Query Match 14.8%; Score 311.5; DB 4; Length 420;  
 Best Local Similarity 26.9%; Pred. No. 9, 9e-19;  
 Matches 100; Conservative 69; Mismatches 156; Indels 47; Gaps 16;

QY 27 DTEIKVNPPODFEIVDPGYLYLQWOPPLSLDHFEKCTVEYELEKYRNGSETWKTITP 86  
 Db 25 DEKISLPPVNFETIKYVG-LAQVLLQWKPNPDQO-RNVNLEYQVKINAKREDDETRET 82  
 QY 87 KNLHYKGFPLNKGIEKHTLLPWCCTNGSGVSSMAETTYWISPOGIEPKYQMDCV 146  
 Db 83 ES--KCVTILHKGFSASVFTILO--NDHSLSSWASAEHL-APGSPGTSVYNLTCT 135  
 QY 147 -----YYNMQYLL-CSMKRGIGVLDTNYNLFY-----WYEGDHALQCVYIKAD 191  
 Db 136 TTTEDNYSRLRSYQVSLHCTWLGTPADPDYQFLFYRRGSWE-----ECGEYAKDT 189  
 QY 192 -GONIGCRFP-VLEASDYKDFYICVNGSSENKPIRSSYTFQLQNIKVP-LPPVYLTFT 248  
 Db 190 LGRNIACMFRTFELISGRDMLAVLVNGSSKSHAIRPFDQFLALHAIQINPLVTAEI 249  
 QY 249 ESSSEIKLKSIPRLGPARGEDYEIEIREDDTTLVTATVENE-TYTLKTNETQQLCFVY 308  
 Db 250 EGT-RLSIQWEKPSAPRIHCFDEYKIHNTNRCYLOIEKIMTNAFSIIDLSKYOV 308  
 QY 309 RSKVNIYCSDDGSIWSEMSDKQCEGDELKSKTLRFMLPFGFILLI-----VIFYTGL 362  
 Db 309 RAAVSSMCREGLMSWMS-QPIYVGNDEHR-LREM-----FVIVMATTCIFILLISLI 361  
 QY 363 LKRPNTYPRKIP 374  
 Db 362 KCIHLMWIKLFP 373

RESULT 6  
 ID Q14631 PRELIMINARY; PRT; 396 AA.  
 AC Q14631;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)  
 DE Interleukin-5 receptor type 2 precursor.  
 GN HSILSR2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NCBI\_TaxID=9606;

[1]  
 SEQUENCE FROM N.A.  
 RC TISSUE-PERIPHERAL BLOOD;  
 RX MEDLINE=92121815; PubMed=1732409;  
 RA Murata Y., Takaki S., Migita M., Kikuchi Y., Tomioka A., Takatsu K.;  
 RT "Molecular cloning and expression of the human Interleukin 5  
 receptor.";  
 RL J. Exp. Med. 175:341-351(1992).  
 DR EMBL: X61177; CAA43484.1; -  
 DR InterPro: IPR002996; CRIA.

[illegible]

Matches	100;	Conservative	57;	Mismatches	142;	Indels	69;	Gaps	19;
QY	53	WQPLSLDHFKECEIYELEKRYN-----IGSTMTKTIITLKHYYDGDGLNKGEIAKIHT	107						
Db	30	WMPEPGAS--PNCITLRYSRSHEDNKODKRIAPET-----HRSKEVPLNRERICLOQWS	78						
QY	108	LLPMQC-TNGSEVOSSMAETTYWISFQIGEPKRYVQDMOCVYYNMQYLLCSNMKPGTIGVLLD	166						
Db	79	-----QCSINESDNPSILYEKC-TTPPEGDPPESAVTELQCVMINLSYMKCTWLPGRNTSPD	133						
QY	167	TNYLNFYWEGLDHALQCVDIKADGONIGREFPY--LEASDYKDFYICVNGSSENKPIR	224						
Db	134	TNYLYLYWHSSHGKILQCED-LYREGQHIGCSFATNLNKDSSFEGHSQIWMYKDNARKIR	192						
QY	225	SSYTFQOLQNYKPLRP-VYLFTFTRESSCEIKLAKSIPUGLTPACQFYETIREDPTT-	282						
Db	193	PSFNIVPLTSHKPPPPPIKRLFFQNGN-LYVQKKNPON-FYSCLSLSYQVEVNNSSQET	249						
QY	283	-----LVTAATVENENYTLKTTNETRQLCFVY-----RSKVAIYC-SDQGLWS	323						
Db	250	NDIFVEEAKQKQNSEF-----EGNLBETICFPMVGVLPDLNTLYRIKVRINKLCEYEDDKLWS	306						
QY	324	EMSDKQCKNEGEDLSKKTLLRFLWLPF-----GFILLYIVTGL--LLRKPMPYR-K	371						
Db	307	NWS-----QAMSIGENIDPTFYITMLATQVAVAGAIITLLLYLRLKIIIFPPIDPDK	361						
QY	372	MIPREFCD 379							
Db	362	IFKEMEGD 369							

RESULT 8	
ID	PRELIMINARY: PRT: 415 AA.
0920K4	
AC	0920K4.
DT	01-MAY-1989 (TREMBLrel. 10, Created)
DT	01-MAY-1989 (TREMBLrel. 10, Last sequence update)
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE	Interleukin-5 receptor alpha precursor.
GN	GPII-SRA.
OS	Cavia porcellus (Guinea pig).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Hystriicongnathi; Cavillidae; Cavia.
OX	NCBI_Taxid=10141;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Norris T.E.;
RT	"Cloning and Characterization of the Guinea Pig Interleukin-5 receptor
RT	alpha cDNA."
RL	Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
DR	EMBL; U55215; AAD09361.1; -.
DR	InterPro; IPR002996; CRIA.
DR	InterPro; IPR003532; Hemtloptn_S_F2.
DR	PROSITE; PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.
KW	Receptor; Signal.
FT	SIGNAL 1 17
FT	CHAIN 18 415
SO	SEQUENCE 415 AA; 46913 MW; 41BA4BA597B31CD4 CRC64;
	POTENTIAL INTERLEUKIN-5 RECEPTOR ALPHA.
	Query Match 14.2%; Score 298.5; DB 11; Length 415;
	Best Local Similarity 26.5%; Pred. No. 1.3e-17;
	Matches 103; Conservative 67; Mismatches 172; Indels 47; Gaps 19
QY	6 LAIGCLYFLISTYTGCGSSDPELKVNPDPDEFIVDPGLYGLYLQWOPRLSDHFKFC 65
DB	7 ILGLGFIQLQDTL-----PDKKFLLLPPINFTKTVG-LAQVVLCEWPNNGO-KKV 58
QY	66 TVEVELKFRNIGSETWKTITKLNHYKGFQDNKGIEAKIHLPLPQCTNGSEVOSSAE 125
DB	59 NLNTHVKINTFOEEIYE---TRNTOSKETTHLQGSVASVRIIL-WH-GHSLASSWVS 112
QY	126 TTYWISPGQIDPEFKVQDMCV-----YNNMQ---YLLCSWKPGIGVLLDTNNALEY 173



Db 113 AEH-KADPSPGSGISVNLCTTNTAASNYNLKSEVSLHCTMLAGDADBDTQFLYYR 171  
Qy 174 ---WEGLDHALQCVYIKAD-GONIGCRFP--YLEASDYKDEYICVNGSSENKPIRSSY 227  
Db 172 YGPRTE-----ECQESKDLISNTACWPPRTFIHSKARDRLAVHNGSSNHAITIPFD 225  
Qy 228 FTFOQLNIVKPLPPVYLFTFRESSCEIKLWKSIPLGPIPARCFDEYIEI-REDDTTLYTA 286  
Db 226 QLFDTQALIDQPNPMDVTAETEGS-RLSIOMQKPVSAFPIHCFEYEVKICITKDYQVEK 284  
Qy 287 TVENETTLKTTNTETROLCTFVVRKKNVICSDDGIMSEMSDKOCBEEDLSKTKLLR-FW 345  
Db 285 TTTNA--FVSTTDGVSXYSIOVRAAVSPHCRAMGLMSKWS-QPYVYQKE--KKPIAGWFL 339  
Qy 346 LPFGFILLIVFVYGLLRKNTYPKMIP 374  
Db 340 ITLTAVLCFIILLIFFELCRITHMTKMP 368

JUL 9  
096BBA PRELIMINARY; PRT; 427 AA.  
AC 096BBA; 08WX08;  
DT 01-DEC-2001 (Tremblrel. 19, Created)  
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
DE 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
DE Interleukin 13 receptor, alpha 1 (BB12804.2.1).  
GN IL13RAL.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=COLON;  
RA Strausberg R.;  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE OF 31-427 FROM N.A.  
RA Lawlor S.;  
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC015768; AAH15768.1; -  
DR EMBL; AL391280; CAD21446.1; -  
DR InterPro: IPR002996; CRA1.  
DR InterPro: IPR003961; FN.III.  
DR InterPro: IPR003532; Hemicoptn\_S\_F2.  
SMART: SM00060; FN3; 1.  
PROSITE: PS01356; HEMATOPO\_REC\_S\_F2; UNKNOWN.1.  
RECEPTOR.  
SQ SEQUENCE 427 AA; 48676 MW; E6AA2F7466A39A09 CRC64;

Query Match 14.1%; Score 297; DB 4; Length 427;  
Best Local Similarity 26.3%; Pred. No. 1.8e-17;  
Matches 110; Conservative 63; Mismatches 172; Indels 74; Gaps 21;

Qy 5 CLAIGC-LYTFILSTFGCTSSDTEIKVNPPODFEYDPGYLGLYLQWOPPLSDHFK 63  
Db 3 CPALCLGIMALLCAGGGGGGGAAPETPTVNLVSVENTCTVLTWMPRGAS--S 60  
Qy 64 ECTVEY-----ELKRYNIGSETWKTIIITKNLHYKDGFDLNGKIGIAKIHLLPMOC-TNGS 117  
Db 61 NCSLMYFSHRGDKODKKIAPETRSI-----EVLNMRICLOQVS---QCSINES 107  
Qy 118 EVOSSAEETIYWIS-POGIPETKYQDMDCVYVNNQYILCSKPGICVILDTNLYLFTWYE 176  
Db 108 EKPSILVEKC--ISPPGDPESAVALTELOCIAMHNLSTYKMSCLPGRNTPSPDNTYLLYYHR 165  
Qy 177 GLDHALQCVYIKADGONIGCRFPYLEASD--YKDFYICVNGSSENKPIRSSYTFOLFON 234  
Db 166 SLEKIHQC-ENIFREGQYFGSFDLTAKYKDSSEFQHSYQIWKNAKIKIKSFNIVPLTS 224  
Qy 235 IVKPLPP-VYLFTRESSCEIKLWKSIPLGPIPARCFDEYIEIREDDTT-----LYTA 286

Db 225 RVKPDPIHKNLSEHND---DLVQWENPQNF1-SRCLFEVEEYVNSQTEETHNVFYQEA 280  
Qy 287 TVENETTLKTTNTETROLCTFV-----RKVNICY-SDGIMSNDKOCWE 332  
Db 281 KCENPEERENVENTS---CEWVPGVLPDPTLNTVIRIKTKNLCEDEDKLMSNSQEM--- 334  
Qy 333 GEDLSKTKLLRFMLPF-----GFLLIVFVYGL--LLRKPNTP-KMIPFECF 379  
Db 335 --SIGKRNSTLYITMILLYPVIVAGAIYLLYLKRLKIIIPFPDPQKIKREMGD 391

RESULT 10  
08VHC2 PRELIMINARY; PRT; 426 AA.  
AC 08VHC2;  
DT 01-MAR-2002 (Tremblrel. 20, Created)  
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)  
DE 01-JUN-2002 (Tremblrel. 21, Last annotation update)  
DE IL-13 receptor alpha 1.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC SRRAIN-FISHER F344;  
RX MEDLINE=21458304; PubMed=11573960;  
RA Pierrot C., Beniguel L., Begue A., Khalife J.;  
RT "Expression of a functional IL-13Ralpha1 by rat B cells.";  
RL Biochem. Biophys. Res. Commun. 287:969-976(2001).  
DR EMBL; AY044251; AAK94870.1; -  
DR InterPro: IPR002996; CRA1.  
DR InterPro: IPR003532; Hemicoptn\_S\_F2.  
DR PROSITE: PS01356; HEMATOPO\_REC\_S\_F2; UNKNOWN.1.  
KW RECEPTOR.  
SQ SEQUENCE 426 AA; 48510 MW; 08BFB0E31D9D3C47 CRC64;

Query Match 14.1%; Score 296; DB 11; Length 426;  
Best Local Similarity 26.1%; Pred. No. 2.2e-17;  
Matches 97; Conservative 56; Mismatches 141; Indels 78; Gaps 17;

Qy 31 KVNPPDFEYDPGYLGLYLQWOPPLSDHFKCTVEY-----ELKRYNIGSETWKTII 85  
Db 28 EVQPPVNLVSVENTCTIWTWMPRGAS--PNCSLRYSHPDQDKIAPETRR--- 82  
Qy 86 TKNLHYKDGFDLNGKIGIAKIHLLPMOC-TNGSEVOSMAETIYISP--OGIPETKYQD 142  
Db 83 -----KKEIPLNKEICLOQVS---QCSINSEKPSPLVKKC--ISPPRG-SESAVTE 129  
Qy 143 MDCVYVNNQYILCSKPGICVILDTNNTLYWYRGDLHALQCVYIKADGONIGCRFPYL 202  
Db 130 LQCTWHLSTYKMSCLWLGKNTSPDNTYLLYWSLSLKSLOC-ENIHREGQIGCSFKLT 188  
Qy 203 EA-SDYKDFYICVNGSSENKPIRSSYTFOLFONIVKPLP-VYLFTFRESSCEIKLMSI 260  
Db 189 KVESNTEHHNIQIWKNAKIKRSYKIVSTSVNKKGPPIKILFLKNGA--LFYQMKN 246  
Qy 261 PLGPIPARCFDEYIEIREDDTT-----LYTAVENE 291  
Db 247 PON-FSSRCLSYEVEAVNSTQDSYNSLSLEVEDKCONSEFDRMMEGASCFISPVILANT 305  
Qy 292 TYTLKTTNTRQLCFVVRKKNVICSDDGIMSEMSDKOCWGEDLSKTKLLRFVLPFGFI 351  
Db 306 VYTVVRVKNKLCF-----DNDLMSNWS-----EALSIGKEPNSTFTYT--ML 348  
Qy 352 LILVIFVYGLLL 363  
Db 349 LILPVFAVYII 360

RESULT 11  
Q15469 PRELIMINARY; PRT; 333 AA.  
ID Q15469

AC Q15469;  
 DT 01-NOV-1996 (Tremblrel. 01, Created)  
 DT 01-NOV-1996 (Tremblrel. 01, last sequence update)  
 DT 01-MAR-2002 (Tremblrel. 20, last annotation update)  
 DE Soluble interleukin-5 receptor precursor.  
 GN HSILSR4.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=PERIPHERAL BLOOD;  
 MEDLINE=92121815; PubMed=1732409;  
 RA Murata Y., Takaki S., Migma M., Kikuchi Y., Tomiwa A., Takatsu K.;  
 RT "Molecular cloning and expression of the human interleukin 5  
 receptor.";  
 RL J. Exp. Med. 175:341-351(1992).  
 DR EMBL: X62156; CA44081.1; -;  
 DR InterPro: IPR002996; CRIA.  
 DR InterPro: IPR003532; Hemtopoptn\_S\_F2.  
 DR PROSITE: PS01356; HEMATOPO\_REC\_S\_F2; UNKNOWN\_1.  
 FT SIGNAL 1 20 POTENTIAL.  
 FT CHAIN 21 333 SOLUBLE INTERLEUKIN-5 RECEPTOR.  
 SQ SEQUENCE 333 AA; 37722 MW; 8D9239845E16985B CRC64;  
 Query Match 13.9%; Score 292; DB 4; Length 333;  
 Best Local Similarity 28.0%; Pred. No. 3 6e-17;  
 Matches 88; Conservative 56; Mismatches 144; Indels 26; Gaps 11;  
 QY 27 DTEIKVNPDPDEFIVDPGYLYLQMPRLSDHFKECTVEYELKYRNIGSETWKTIIT 86  
 DB 25 DEKISLPVPNFTIKYVG-LAQVLLQKPNPDQO-RNVNLEQVKNAPKEDDEYERIT 82  
 QY 87 KNLHYKGFPLNGIEKINHTLTPMOCTNGSEVOSSMAETTYWISPGIGETKYQMDCV 146  
 DB 83 ES---KCVTLHKGFSASVFTILO---NDHSLASSWASAEHL-APGSPGTSTVNLCT 135  
 QY 147 -----YNNQYL-CSMKPGIGVLLDTNVLNFWYEGDLHALQCVYIKAD-GON 194  
 DB 136 TMTEDNYSRLRSQVSLHCTWLTGTPADPDQYFLYYRGSWTE--ECOEYSKDTIGRN 193  
 QY 195 IGRFP--YLEASDYKDFYICVNGSSSENKPIRSSYFTFQLOINIKPLPYVYLFTRESSC 252  
 DB 194 IACWFPRTFLSKGRDVLAVLVNGSSKHSARPEDDQLFALHAIDQINPNTVAEIGT- 252  
 QY 253 EIKKMSIPLGPIPARCFDEYIEIRREDDTLVATVENEYTLKTNETQOLCFVARSKY 312  
 DB 253 RLSTQWKPVSAPFPHCFDEYEVKIHNTNGYLOIEKIMTNAFISIDLSKYDVQVRAAV 312  
 QY 313 NIYCSDDGINSSEWS 326  
 DB 313 SSMCREAGLSSEWS 326  
 RESULT 12  
 Q920B8 PRELIMINARY; PRT; 414 AA.  
 AC Q920B8;  
 DT 01-DEC-2001 (Tremblrel. 19, Created)  
 DT 01-MAR-2001 (Tremblrel. 19, last sequence update)  
 DT 01-MAR-2002 (Tremblrel. 20, last annotation update)  
 DE Interleukin-5 receptor alpha.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Rattus.  
 OC NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=E344;  
 RA Pierrot C., Begue A., Szpirer C., Capron A., Capron M., Khalife J.;  
 "Molecular cloning and characterization of rat IL-5 $\alpha$  gene."

RT chromosomal mapping, analysis of the 5'-upstream region and expression  
 by B cells.";  
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF24153; AAK97344.1; -;  
 DR InterPro: IPR002996; CRIA.  
 DR InterPro: IPR003532; Hemtopoptn\_S\_F2.  
 DR PROSITE: PS01356; HEMATOPO\_REC\_S\_F2; UNKNOWN\_1.  
 KW Receptor.  
 SQ SEQUENCE 414 AA; 47075 MW; 4340F42P47297D84 CRC64;  
 Query Match 12.7%; Score 268; DB 11; Length 414;  
 Best Local Similarity 26.0%; Pred. No. 5.5e-15;  
 Matches 103; Conservative 64; Mismatches 151; Indels 78; Gaps 20;  
 QY 17 STEFGCTSSDTEIKVNPDPDEFIVDPGYLYLQMP-----PLSDHFKECTVEYEL 71  
 DB 12 SATLHADLLSPKFKLLPVPNFTIKATG-LAQVPLHNDPDPDQVPLKHYVKNPQED 70  
 QY 72 KYRNIGSETWKTIITKNLHYKGFPLNGIEKINHTLTPMOCTNGSEVOSSMAETTYWIS 131  
 DB 71 EYD-----TKNTESKCVTPLHEGFAASVFTILK---SIHSPLASWVASAEHL-KA 115  
 QY 132 PGIGETKYQMDCV-----YNNQY-LCSMKPGIGVLLDTNVLNFW-----WYE 176  
 DB 116 PPGSSGTSVNNLCTTNTVKSHTFHRPYQVSLRCTLVWKDAPEDQYFLYYRFSWTE 175  
 QY 177 GLDHALQCVYIK-ADGONIGCRFP--YLEASDYKDFYICVNGSSSENKPIRSSYFTFQ 233  
 DB 176 -----ECOEYSKDALNRNACNFPRTFINSKGFQDLAVINSSKHAATKPLDQFTLY 229  
 QY 234 NIVKPLPVPYVLTFTRESSCEIKLWMSIPLGPIPARCFDEYIEIRDDT-----TLVT-- 285  
 DB 230 AIDQVNPVNVVTEIERN-SLYIOMGKPLSAPVHCKKYLKTYNKGYSQEMNLVTNK 288  
 QY 286 -ATVEN-ETTYLKTNETQOLCFVARSKNITCSDDGINSSEWSDKQWGEDLSKLTLL 342  
 DB 289 FISKIDVSTYSIQ-----VRAAVSSPCRRSGSGSEWS-PTIYVK---KKPL 333  
 QY 343 RFW---LPEGFLLIVFVTGLLRKPNTPYKMP 374  
 DB 334 VEWHLIVLPALICFILIF--SLICRYHLMTRLF 367  
 RESULT 13  
 Q97597 PRELIMINARY; PRT; 349 AA.  
 AC Q97597;  
 DT 01-MAY-1999 (Tremblrel. 10, Created)  
 DT 01-MAY-1999 (Tremblrel. 10, last sequence update)  
 DT 01-MAR-2002 (Tremblrel. 20, last annotation update)  
 DE Interleukin-13 receptor alpha-1 chain (Fragment).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OC NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=20080132; PubMed=10614495;  
 RA Trigona W.L., Brown W.C., Estes D.M.;  
 RT "Functional implications for signaling via the IL4R/IL13R complex on  
 bovine cells.";  
 RL Vet. Immunol. Immunopathol. 72:73-79(1999).  
 DR EMBL: AF074402; AAC98147.1; -;  
 DR InterPro: IPR002996; CRIA.  
 DR InterPro: IPR003532; Hemtopoptn\_S\_F2.  
 DR PROSITE: PS01356; HEMATOPO\_REC\_S\_F2; UNKNOWN\_1.  
 KW Receptor.  
 FT NON\_TER 1 1  
 FT TER 349 349  
 SQ SEQUENCE 349 AA; 39644 MW; D61A4C918B1940A6 CRC64;  
 Query Match 12.6%; Score 264.5; DB 6; Length 349;



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GenCore version 5.1.3  
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OM protein - protein search, using SW model

Run on: January 24, 2003, 19:34:59 ; Search time 21 Seconds  
(without alignments)  
1739.575 Million cell updates/sec

Title: US-09-714-792a-4

Perfect score: 2104  
Sequence: 1 MAFVCIAGICLYTFLISTTF.....LLRRPNTPYKMIPEFCDT 380

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Archived: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	311.5	14.8	420	2	JC21052 IL-13Ra1pha-5 rece
2	296	14.1	426	2	JC7773 IL-13Ra1pha-1 prot
3	292	13.9	335	2	A40267 interleukin-5 rece
4	263	12.5	831	2	UQ1655 prolactin receptor
5	247	11.7	415	2	S12357 interleukin-5 rece
6	230	10.5	369	2	A42565 interleukin-2 rece
7	216.5	10.3	830	2	I50455 prolactin receptor
8	212.5	10.1	369	2	I49280 interleukin-2 rece
9	208	9.9	373	2	A55718 interleukin-2 rece
10	195	9.3	878	1	A40091 interleukin-3 rece
11	180.5	8.6	897	1	A39255 cytokine receptor
12	178	8.5	896	2	I56563 interleukin-3 rece
13	173.5	8.2	896	1	A35782 cytokine receptor
14	165	7.8	310	2	A29884 prolactin receptor
15	165	7.8	412	2	A41070 prolactin receptor
16	165	7.8	581	2	A45971 prolactin receptor
17	165	7.8	610	2	A34631 prolactin receptor
18	165	7.6	610	2	A36116 prolactin receptor
19	160.5	7.6	303	2	I77524 prolactin receptor
20	159	7.6	292	2	I77525 prolactin receptor
21	159	7.6	608	2	I53269 prolactin receptor
22	151	7.2	288	2	B59405 prolactin receptor
23	151	7.2	376	2	A59405 prolactin receptor
24	151	7.2	622	2	A40144 prolactin receptor
25	150.5	7.2	917	2	I49699 glycoprotein 130 -
26	149	7.1	616	2	A30304 prolactin receptor
27	142.5	6.8	400	2	S06945 granulocyte-macrop
28	138	6.6	378	2	A40266 interleukin-3 rece
29	134.5	6.4	1097	2	S17308 leukemia inhibitor

30	133.5	6.3	333	2	S13684 granulocyte-macrop
31	133.5	6.3	378	2	S50040 granulocyte-macrop
32	131.5	6.2	630	2	I51086 prolactin receptor
33	129	6.1	150	2	B34631 lactogen receptor
34	126.5	6.0	918	2	A36337 membrane glycoprot
35	122.5	5.8	286	2	S50039 granulocyte-macrop
36	120.5	5.7	771	2	B38252 granulocyte colony
37	120.5	5.7	783	2	JH0329 granulocyte colony
38	120.5	5.7	863	2	C38252 granulocyte colony
39	112.5	5.3	1630	2	C41214 protein-tyrosine-p
40	111.5	5.3	1557	2	D41214 protein-tyrosine-p
41	110	5.2	6805	2	S20901 titin - rabbit (fr
42	109.5	5.2	918	2	A44257 interleukin-6 sign
43	109.5	5.2	26926	1	I138344 titin, cardiac mus
44	107.5	5.1	638	2	A33991 somatotropin recep
45	107.5	5.1	837	2	A34898 granulocyte colony

## ALIGNMENTS

RESULT 1  
S21052  
Interleukin-5 receptor alpha chain precursor (clone lambda h5R.12), membrane-anchored  
C:Species: Homo sapiens (man)  
C:Date: 22-Nov-1993 #sequence-revision 10-Nov-1995 #text-change 01-Dec-2000  
C:Accession: S21050: S21050: S21053: A46175: S78106: S78107  
R:Murata, Y.; Takaki, S.; Migita, M.; Kikuchi, Y.; Tomimaga, A.; Takatsu, K.  
J. Exp. Med. 175, 341-351, 1992  
A:Title: Molecular cloning and expression of the human interleukin 5 receptor.  
A:Reference number: S21050; MID:92121815; PMID:1732409  
A:Accession: S21052  
A:Molecule type: DNA  
A:Residues: 1-420 <MU>  
A:Cross-references: EMBL:X61176; NID:g33843; PIDN:CAA43483.1; PID:g33844  
A:Experimental source: clone lambda h5R.12  
A:Accession: S21050  
A:Molecule type: DNA  
A:Residues: 1-395, 'I', <MU2>  
A:Cross-references: EMBL:X61177; NID:g33839; PIDN:CAA43484.1; PID:g33840  
A:Experimental source: clone lambda h5R.27  
A:Accession: S21053  
A:Molecule type: mRNA  
A:Residues: 1-332, 'K', <MU3>  
A:Cross-references: EMBL:X62156; NID:g36465; PIDN:CAA44081.1; PID:g36466  
A:Experimental source: clone lambda h5R.25  
R:Tavernier, J.; Tuypens, T.; Platek, G.; Verhee, A.; Fiers, W.; Devos, R.  
Proc. Natl. Acad. Sci. U.S.A. 89, 7041-7045, 1992  
A:Title: Molecular basis of the membrane-anchored and two soluble isoforms of the hum  
A:Reference number: A46175; MID:92357767; PMID:1495999  
A:Accession: A46175  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 333-420 <TA>  
A:Experimental source: HL-60 cells and eosinophils  
A:Note: sequence extracted from NCBI backbone (NCBIN:116243, NCBI:116244)  
R:Murata, Y.  
submitted to the EMBL Data Library, July 1991  
A:Reference number: S78106  
A:Accession: S78106  
A:Molecule type: DNA  
A:Residues: 1-128, 'I', 130-395, 'I', <MUW>  
A:Cross-references: EMBL:X61177; NID:g33839; PIDN:CAA43484.1; PID:g33840  
R:Murata, Y.  
submitted to the EMBL Data Library, September 1991  
A:Reference number: S78107  
A:Accession: S78107  
A:Molecule type: mRNA  
A:Residues: 1-128, 'I', 130-332, 'K', <MU4>  
A:Cross-references: EMBL:X62156; NID:g36465; PIDN:CAA44081.1; PID:g36466  
C:Keywords: alternative splicing; cytokine receptor; glycoprotein; transmembrane prot  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-420/Product: interleukin-5 receptor alpha chain #status predicted <MAT>



A:Cross-references: DDBJ:D13154; NID:g222848; PID:BA02439.1; PID:g222849  
 A:Experimental source: kidney  
 A:Superfamily: cytokine receptor homology  
 C:Keywords: glycoprotein; transmembrane protein  
 F:123/Domain: signal sequence #status predicted <SIG>  
 F:24-831/Product: prolactin receptor #status predicted <MAT>  
 F:36-219/Domain: cytokine receptor homology <CRS1>  
 F:239-425/Domain: cytokine receptor homology <CRS2>  
 F:439-462/Domain: transmembrane #status predicted <TM>  
 F:59,91,100,112,132,262,303,315,335,647,701,800/Binding site: carbohydrate (asn) (covale

Query Match 12.5%; Score 263; DB 2; Length 831;  
 Best Local Similarity 26.4%; Pred. No. 7.6e-13;

Matches 103; Conservative 58; Mismatches 183; Indels 46; Gaps 17;

18 TTTCCTSSDTEIKVN--PQDFE---LVDPG-----YLGYLQWQPLSL 59  
 97 TTFMTVATANEIGSSSDPQYDVTSIVOPGSPVNLLETGRSANIMYLMAKSPPLA 156  
 60 DHEKCTVEYELKRYNIGSETWKTIIIRKHLHYKDFDLNKGIEAKIHITLPMQCTNGSEV 119  
 157 DASNHLHYELRIKPEPEKEMETI---SVGVQCKINR-LNAGMRYVAVGCTLDIGE 212  
 120 QSSWAETTYWISPG-IPETKVQDMDCVYVNMWYLLCSWPKIGVLLDTNINLEFYWEGL 178  
 213 WSEWSEBRHILIPSGQSPREKPTIIKCRSPKEFTFCMMKRGDGGHPTNTLLYSKEGE 272  
 179 DHALQCDYIKADQONIGCRPYLEASDYKDFYICVWSSNKRITRSYTFQLONIYKP 238  
 273 EQVEECDDY-RTAGPN-SCYFDKHKTSFWITVNTVATNIGSSSPHVDVYIVOP 330  
 239 LPVYLYFTFRESSCEIK-----LKWS-IPLPPIPARCFDYEIFEIR---EDDTLTATAVEN 290  
 331 DPEVNTVLELKKRPILNRPYLVLTSPPLADYRSGWLTLELELKKDEGEMETITVGO 390  
 291 ET-VTLKTNETQQLCEVVRKVNIVYSDS--GIWSEMSDKQCE--GEDLSKTKTLRFL 346  
 391 OTQYKMSLNNGKKYI-----IQHCKRPHHGSWSESSNNTYIQINDPEVVKMI-VWI 443  
 347 PFGPI-LIIVIFVTGILLKRPNTPKMIP 374  
 444 VLGVLSSLICLIMSWTLVKGMYTFLMP 473

## RESULT 5

S12357

Interleukin-5 receptor - mouse  
 Species: Mus musculus (house mouse)

C:Date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 20-Jun-2000  
 C:Accession: S12357

R:Takaki, S.; Tomlinaga, A.; Hltoshi, Y.; Mita, S.; Sonoda, E.; Yamaguchi, N.; Takatsu, K.

EMBO J. 9, 4367-4374, 1990

A:Title: Molecular cloning and expression of the murine interleukin-5 receptor.

A:Reference number: S12357; MUID:91092260; PMID:2265612

A:Accession: S12357

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-415 <TAK>

A:Cross-references: GB:D90205; NID:g220465; PIDN:BA01231.1; PID:g220466

C:Keywords: cytokine receptor; transmembrane protein

Query Match 11.7%; Score 247; DB 2; Length 415;  
 Best Local Similarity 24.6%; Pred. No. 5.8e-12;

Matches 91; Conservative 70; Mismatches 151; Indels 58; Gaps 18;

34 PQDFEIVDPGYLGLYLQWQPLSLDHFKECTVEYELKRYNIGSETWKTIIIRKHLKYD 93  
 29 PVNFTIKANG-LAQVLLHMDPNPDQEQ-RHVDLEYHKINAPQDEYDFRKTES---KC 83  
 94 GFDLNRKIEAKIHITLPMQCTNGSEVQSSWAETTYWISPGIPETKVQDMDCVYVNMWYLLC 149  
 84 VTPLEHGFASVRIILK---SSHITLASSWVSAEL-KAPPGSPGTSVNTLCTHTVAVSS 139

150 -----MOY-LLCSWPKIGVLLDTNINLEFYWEGLDHALQCDYIK-ADQONIGCRPP- 200  
 140 HTHLRPYQVSLRCTLWLVGKADPEDTQYFLYRFEGLVE--KQGEYKRALNRNACWFP 197  
 201 -YLEASDYKDFYICVWSSNKRPIRSSYTFPQLONIYKPLPVLYFTFRESSCEIKLWS 259  
 198 TFINSGFQGLAVHINSSKRAAIKPPDQFLSPALIDQVNPFRVATYEEN-SLYIQWE 256  
 260 IPLCPPIARCFDYEIFEREDD-----TTLVATVAVENEFYTLKTNETQQLCEV 308  
 257 KPLSAPFDHCFENYELKRYNIGSETWKTIIIRKHLHYKDFDLNKGIEAKIHITLPMQCTNGSEV 305  
 309 RSKVNIYCSDDGISEMSDKQCEGEDLSKTKTLRFW---LPPGILLIIVIFVTGILLR 364  
 306 RAAVSPFCRMPGRGEMS-QPIYVGEK--KSLAVE-NHLIVLPYACFVLLIF--SLICR 359  
 365 KPNTPPKMIP 374  
 360 VCHLMTRLFP 369

## RESULT 6

A42565

Interleukin-2 receptor gamma chain - human

C:Species: Homo sapiens (man)

C:Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 20-Jun-2000

C:Accession: A42565; A46591; I54332

R:Takeshita, T.; Asano, H.; Ohtani, K.; Ishii, N.; Kumaki, S.; Tanaka, N.; Munakata, H.

Science 257, 379-382, 1992

A:Title: Cloning of the gamma chain of the human IL-2 receptor.

A:Reference number: A42565; MUID:92335883; PMID:1631559

A:Accession: A42565

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid; protein

A:Residues: 1-369 <TAK>

A:Cross-references: GB:U11086; NID:g303611; PIDN:BA01857.1; PID:g219890

A:Experimental source: MOLF beta lymphoid cells

A>Note: sequence extracted from NCBI backbone (NCBI:109167)

R:Noguchi, M.; Adelstein, S.; Cao, X.; Leonard, W.J.

J. Biol. Chem. 268, 13601-13608, 1993

A:Title: Characterization of the human interleukin-2 receptor gamma chain gene.

A:Reference number: A46591; MUID:93293887; PMID:8514792

A:Accession: A46591

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-369 <RES>

A:Cross-references: GB:U12183; NID:g307056; PIDN:AAA59145.1; PID:g307058

R:Puck, J.M.; Deschenes, S.M.; Porter, J.C.; Dutra, A.S.; Brown, C.J.; Willard, H.F.; Hum. Mol. Genet. 2, 1099-1104, 1993

A:Title: The interleukin-2 receptor gamma chain maps to Xq13.1 and is mutated in X-11

A:Reference number: I54332; MUID:94004847; PMID:8401450

A:Accession: I54332

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-369 <RES2>

A:Cross-references: GB:U19546; NID:g349631; PIDN:AAC37524.1; PID:g349632

C:Genetics:

A:Gene: GDB:112RG; SCIDX1, IMD4

A:Cross-references: GDB:134807; OMIM:308380

A:Map position: Xq13.1-Xq13.1

A:Introns: 39/1; 90/2; 152/3; 198/3; 253/1; 285/2; 308/3

A>Note: defects are associated with an X-linked form of severe combined immunodeficiency

C:Superfamily: interleukin-2 receptor gamma chain

C:Keywords: cytokine receptor; duplication; immunodeficiency; severe combined immunod

Query Match 10.5%; Score 220; DB 2; Length 369;  
 Best Local Similarity 25.5%; Pred. No. 6.9e-10;  
 Matches 70; Conservative 48; Mismatches 121; Indels 36; Gaps 11;

97 LNKGIEAKIHITLPMQCTNGSE-VQSSWAETTYWISPGIPETKVQDMDCVYVNMWYLLC 155  
 19 LGVGLNTIILT-----PNGNEDYTADEFLLTMTDLSLSTLPLPEVQCFVFNVEYVNC 72

[illegible]

C:Date: 27-Feb1997 #sequence revision 27-Feb-1997 #text.change 20-Jun-2000  
A:Accession: 149280; A47514; UN0775; S37582; I53398  
R:CaO, X.; Kozak, C.A.; Liu, Y.  
Proc. Natl. Acad. Sci. U.S.A. 90, 8464-8468, 1993  
A:Title: Characterization of cDNAs encoding the murine interleukin 2 receptor (IL-2R)  
A:Reference number: A47514; MUID:9391374; PMID:8378320  
A:Accession: 149280  
A:Status: preliminary; translated from GR/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-369 <CAO>  
A:Cross-references: EMBL:U21795; NID:9727349; PIDN:AA64279.; PID:9727350  
A:Accession: A47514  
A:Status: translated from GR/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-369 <RE>  
A:Cross-references: GB:L20048; NID:9404067; PIDN:AAA39286.1; PID:9404068  
R:Kunakl, S.; Kondo, M.; Takashita, T.; Asao, H.; Nakamura, M.; Sugamura, K.  
Biochem. Biophys. Res. Commun. 193, 356-363, 1993  
A:Title: Cloning of the mouse interleukin 2 receptor gamma chain: Demonstration of fu  
A:Reference number: JN0592; MUID:93277575; PMID:8503926  
A:Accession: JN0592  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-369 <KIM>  
A:Cross-references: DDBJ:D13565; NID:9303684; PIDN:BAA02760.1; PID:9303685  
R:Kobayashi, N.; Nakagawa, S.; Minami, Y.; Taniguchi, T.; Kono, T.  
Gene 130, 303-304, 1993  
A:Title: Cloning and sequencing of the cDNA encoding a mouse IL-2 receptor gamma.  
A:Reference number: JN0775; MUID:93366191; PMID:8359659  
A:Accession: JN0775  
A:Molecule type: mRNA  
A:Residues: 1-369 <KOB>  
A:Cross-references: GB:D13821; NID:9436045; PIDN:BAA02974.1; PID:9436046  
R:Chiu, R.K.; Dougherty, G.J.  
submitted to the EMBL Data Library, October 1993  
A:Description: Regulation of CD4-mediated cellular adhesion by the IL-2 R gamma chain  
A:Reference number: S37582  
A:Accession: S37582  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-350, 'S', 352-366, 'S', 368-369 <CHI>  
A:Cross-references: EMBL:X75337  
R:Disanto, J.P.; Certain, S.; Wilson, A.; MacDonald, H.R.; Avner, P.; Fischer, A.; de  
Eur. J. Immunol. 24, 3014-3018, 1994  
A:Title: The murine interleukin-2 receptor gamma chain gene: organization, chromosoma  
A:Reference number: I53398; MUID:95104285; PMID:7805729  
A:Accession: I53398  
A:Status: preliminary; translated from GR/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-369 <RES>  
A:Cross-references: GB:S75852; NID:9861554; PIDN:AAB32904.1; PID:9861555  
A:Accession: I53398  
A:Gene: IL-2Rgamma  
A:Introns: 39/1; 90/2; 152/1; 199/3; 254/1; 286/2; 308/3  
A:Complex: The high affinity receptor is a heterotrimer of alpha (see PIR:UHMS2), bet  
eptors.  
C:Function:  
A:Description: receptor for interleukin-2  
A:Pathway: interleukin-2 stimulated growth and differentiation of T cells, B cells, N  
C:Superfamily: interleukin-2 receptor gamma chain  
C:Keywords: cytokine receptor; duplication; glycoprotein; transmembrane protein  
F:1-22/Domain: signal sequence #status predicted <SIG>  
F:23-369/Product: interleukin-2 receptor gamma chain #status predicted <MAT>  
F:256-284/Domain: transmembrane #status predicted <TM>  
F:71,75,84,96,159,164,306/Binding site: carboxyrate (Asn) (covalent) #status predict



A:Molecule type: mRNA  
A:Residues: 1-878 <IT0>  
R:Gorman, D.M.  
submitted to GenBank, November 1989  
A:Reference number: A43022  
A:Accession: A43022  
A:Molecule type: mRNA  
A:Residues: 1-815, 'Q', 817-878 <GOR>  
A:CROSS-references: GB:M29855; MID:g198342; PIDN:AAA3295.1; PID:g039406  
C:Comment: In mice there are two classes of high-affinity IL-3 receptors. One contains receptors.

C:Superfamily: interleukin-3 receptor beta chain: cytokine receptor homology  
C:Keywords: cytokine receptor; duplication; transmembrane protein  
F:1-32/DNA: signal sequence #status predicted <SIG>  
F:23-878/Product: Interleukin-3 receptor beta chain #status predicted <MAT>  
F:23-440/DNA: extracellular #status predicted <EXT>  
F:39-236/DNA: cytokine receptor homology <CRS1>  
F:254-433/DNA: cytokine receptor homology <CRS2>  
F:441-462/DNA: transmembrane #status predicted <TM>  
F:463-878/DNA: intracellular #status predicted <INT>

Query Match 9.3%; Score 195; DB 1; Length 878;  
Best Local Similarity 24.1%; Pred. No. 2e-07;  
Matches 86; Conservative 59; Mismatches 150; Indels 62; Gaps 23;

OY 34 PPDFEIVDPGYGLYLQMOPPL---SLDHKECTVEYELKYNIGSEPMKTITTKLH 90  
||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:  
Db 139 PKDHIHSFG--DHFLLEMSVSLGDSQVSWLSKDIEFEVAKYRL--ODSMED--ASSLIH 193  
  
OY 91 YKDGDLNKGTIAKHHTLLP-----WQCTNGSEVQ---SSAAETWTMSPGIRET 138  
| | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | :  
Db 194 -TSNQVN--LEPKL--FLPNSTIARVRTRLSAGSSLSGRPSRNSPEVHMDSOPG-DKA 247  
  
OY 139 KYVDMDCVYYNNQVLYLCGSKPGIGVLDTNYMLFYWEGDLHALQCVDYIKADGONI--- 195  
| | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | :  
Db 248 GPQNQLCCFFDGIQSILHCSEWVTOTGSVPFLFRPSPAAREEKCSVVAEPAQSVYTR 307  
  
OY 196 -GCRRPYLEASDYKDFYICVNGSSSENKPIRSYTFPQLONIYKPLPVY-LTTRESSCE 253  
| | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | :  
Db 308 YRCSPJPEPESAHSQYTSAVKLEQGKF-MSYVHIQME-----PLLNTOKNRDS--- 357  
  
OY 254 IKLKMSIPLGPIAPACFD--YEIEIREDDTLVTATVEN----EYTIKLTNEPQOLFV 307  
| | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | :  
Db 358 YSLHMETOKIP--YYIDHTEFVQYKKRSSESKSDKTEKLGVNSMDP:PQLEPDPTSYCAR 414  
  
OY 308 VRSK-VNIKXSDGIMSEWDKOCWGEDLSKRTLEFLPGFILLIVIFVYGILL 363  
| | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | :  
Db 415 VAVKPISDY---DGIWSENSNEYMT-IDWVWPFL---WI-----VLIVFLILFTLLL 460

RESULT 11  
A39255  
cytokine receptor common beta chain precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 02-Sep-1997  
C:Accession: A39255  
C:Accession: A39255  
R:Hayashida, K.; Kitamura, T.; Gorman, D.M.; Arai, K.; Yokota, T.; Miyajima, A.  
Proc. Natl. Acad. Sci. U.S.A. 87, 9655-9659, 1990  
A:title: Molecular cloning of a second subunit of the receptor for human granulocyte  
A:Reference number: A39255; MUID:91088571; PMID:1702217  
A:Accession: A39255  
A:Molecule type: mRNA  
A:Residues: 1-897 <HAY>  
A:CROSS-references: GB:M38275  
C:Comment: The human high-affinity IL-3, IL-5, and GM-CSF receptors have ligand-specific  
C:Genetics:  
A:Gene: GDB:CSF2RB  
A:CROSS-references: GDB:126838; OMIM:138981  
A:Map position: 22q13.1-22q13.1  
C:Superfamily: interleukin-3 receptor beta chain: cytokine receptor homology  
C:Keywords: alternative splicing; cytokine receptor; duplication; transmembrane protease  
F:1-16/DNA: signal sequence #status predicted <SIG>  
F:17-897/Product: cytokine receptor common beta chain #status predicted <MAT>

F:17-443/Domain: extracellular #status predicted <EXT>  
F:33-233/Domain: cytokine receptor homology <CRS1>  
F:250-431/Domain: cytokine receptor homology <CRS2>  
F:444-460/Domain: transmembrane #status predicted <TM>  
F:461-897/Domain: intracellular #status predicted <INT>

Query Match 8.6%; Score 180.5; DB 1; Length 897;  
Best Local Similarity 22.6%; Pred. No. 2.9e-06;  
Matches 90; Conservative 58; Mismatches 146; Indels 105; Gaps 21;

QY 32 VNPQDEFIVPGYLG-----LYLQMP-----LSLDP----- 62  
DB 97 VIFQSEVYVDYFSPQPRPLGLTVTLTQHVQPEPPDLQISTQDHFLLTWVAL 156  
QY 63 -----KECTVEELKYNIGSETWK--TITKNLHYKDGFLNKIG-----A 103  
DB 157 GSPQSHMLSPEDLEFVYKRL-QDSMEDAILSLNTS-----QATLGEPLHMSRTYVA 210  
QY 104 KIH-LLPQCTNGSEVQSSAETTYWISPOGIPETKYQDMCVYNNQVLLCSKKPGIG 162  
DB 211 RVRTPLAPGSLRSGR--PSKWSPEVCWDSQPG-DEAOPQNECFEDGAVALSCSWEVAK 267  
163 VLLDTNVLFFWYEGDLHALQCVDIKADGONIG-----CRFPYLEASDYKDFYICVN 215  
DB 268 VASSVSSELFKPSPDAGEECSPVLR--EGLSLTRHHKQIPVDPATHGQIVSVQ 324  
QY 216 GSSENKPIRSSYFTFQLONIYKPLPPVYLFTFRSSCEIKLWSIPLGPIPARCFDYEIE 275  
DB 325 PRAEKKHKSSV-----NI--QMAPSLANTKQGD--SYSLRWETMKMRYEHIDHTEFIQ 375  
QY 276 IREDDTLVATV-VENEYTYLTKTN-----ETROLCEV-VRSKVNICYSDGCIWSE 324  
DB 376 YRKD-----TATMKDSKTETIQNAHSMALPALPSTRYMAVRVTSRTGY---NGIWE 427

## RESULT 12

156563  
Interleukin-3 receptor beta-subunit - rat  
C:Species: Rattus sp. (rat)  
C>Date: 26-Jul-1996 #sequence, revision 26-Jul-1996 #text, change 23-Jul-1999  
C:Accession: 156563  
R:Appel, K.; Buttin, M.; Sauter, A.; Gebicke-Haerter, P. J.  
J. Neurosci. 15, 5800-5809, 1995  
A:Title: Cloning of rat interleukin-3 receptor beta-subunit from cultured microglia and  
A:Reference number: 156563; MUID:95370942; PMID:7643220  
A:Accession: 156563  
A:Status: preliminary; translated from GB/EMBL/DDAJ  
A:Molecule type: mRNA  
A:Residues: 1-896 <RES>  
A:Cross-references: GB:579263; NID:g1086954; PIDN:AA835068.1; PID:g1086955  
C:Genetics:  
A:Gene: IL-3beta  
C:Superfamily: Interleukin-3 receptor beta chain; cytokine receptor homology  
C:Keywords: cytokine receptor  
F:33-235/Domain: cytokine receptor homology <CRS1>  
F:253-433/Domain: cytokine receptor homology <CRS2>

Query Match 8.5%; Score 178; DB 2; Length 896;  
Best Local Similarity 21.4%; Pred. No. 4.6e-06;  
Matches 87; Conservative 65; Mismatches 167; Indels 88; Gaps 21;

QY 5 CLAIGCL-VN-FLISTFGCTSSDMEIKVN-----PQDFELVDPGYLGYL 49  
DB 94 CVPRRCVLPYQVSSEEDYSLQPDRLSLHLVPLAQHVQPPPKDISISPG--DHF 151  
QY 50 YLQMPPL--SLDHFRECTVEELKYNIGSETWKTITTKNLHYKQGFNDKIEAKIH 106  
DB 152 LTKSVPLGDQVSLLSQKDLQEFVAKQL-QDSMED--ASSLH-----TCNLAVTLEPK 203

QY 107 TLPP-----NQTNGSEVQ--SSMAETTYWISPOGIPETKYQDMCVYNNQVLL 154  
DB 204 LFLNLSIVARVRAQLAPGSSLSGRPSGMSPEVHSDPTE--DKARPQLQCFQFQIGSL 262  
QY 155 CSMPKPGICVLDITVNNLFYWEGLDHALQCVDIKADGONIGCFPIYLEADYDFYICV 214  
DB 263 CSWEWTKRVDSVSFGLFSSSPKAGEKKCSPVKE-----LQASRYRYICSL 311

QY 215 NGSENKPIRSSYFTFQLO-----NIKRVLP-YYLFTFRSSCEIKLWSIPL 262  
DB 312 NVSD--PAHSQYTVSVKRLDQKGFIESFNHQMNPPLTLTKNRDS---YSLHMETQK 365  
QY 263 GPIPARCFDYEIEIR-----EDDTLVATVAVENETYLTKTNETROLCEVRSKVNICY 316  
DB 366 MSYPIHAFQVQYKKKLDREWDSKT-----ENLHAHSMDLPOLEPGSYCARVAVTIP 421  
QY 317 SDDISWRSKQCEGEDLSKTLRFWLPFGILLIIVITGILL 363  
DB 422 EYKGLWSEMSNECWT-TDWVMPPL--WI--VLILVFLILFLL 460

## RESULT 13

A35782  
Cytokine receptor common beta chain precursor - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 30-Jun-1993 #sequence, revision 30-Jun-1993 #text, change 22-Jun-1999  
C:Accession: A35782  
R:Gorman, D.M.; Itoh, N.; Kitamura, T.; Schreurs, J.; Yonehara, S.; Yahara, I.; Araki, A.  
Proc. Natl. Acad. Sci. U.S.A. 87, 5459-5463, 1990  
A:Title: Cloning and expression of a gene encoding an interleukin 3 receptor-1like pro  
A:Reference number: A35782; MUID:90319131; PMID:1695379  
A:Accession: A35782  
A:Molecule type: mRNA  
A:Residues: 1-896 <GOR>  
A:Cross-references: GB:M34397; NID:g191821; PIDN:AA37204.1; PID:g309101  
C:Comment: Mouse high-affinity IL-5, GM-CSF, and one class of high-affinity IL-3 rece  
C:Superfamily: Interleukin-3 receptor beta chain; cytokine receptor homology  
C:Keywords: cytokine receptor; duplication; transmembrane protein  
F:1-22/Domain: signal sequence #status predicted <SIG>  
F:23-896/Product: cytokine receptor common beta chain #status predicted <MAT>  
F:23-441/Domain: extracellular #status predicted <EXT>  
F:33-235/Domain: cytokine receptor homology <CRS1>  
F:253-434/Domain: cytokine receptor homology <CRS2>  
F:442-463/Domain: transmembrane #status predicted <TM>  
F:464-996/Domain: intracellular #status predicted <INT>

Query Match 8.2%; Score 173.5; DB 1; Length 896;  
Best Local Similarity 20.7%; Pred. No. 1e-05;  
Matches 81; Conservative 69; Mismatches 185; Indels 57; Gaps 18;

QY 5 CLAIGCLVTFPLISTFGCTS-----SSDPEIK-----VNPQDEFIVDPGYLG 48  
DB 94 CVPRRCVLPY---TRFSTINDEYVSFRPDSGLQWLAVPLAQNVQPPPLKVNSSSEDR 150  
QY 49 LYLQMPPL--SLDHFRECTVEELKYNIGSETWKTITTKN-----LHYKGFNDKNG 100  
DB 151 FILEMSVSLGDAQVSWLSKDIIEFVAVKRL-QDSMEDAVSLHRSKFOVNEPFLPNS 209  
QY 101 IEA-KIH-LLPQCTNGSEVQSSAETTYWISPOGIPETKYQDMCVYNNQVLLCSWK 158  
DB 210 IYAPRVTRLPYGSLSGR--PSKWSPEAHWDSPG-DKAPQWLQCFQIGSLHCSWE 266  
QY 159 PGICVLLDTNVLNLFYWEGLDHALQCVDIK-ADGONI-----GCRFPYLEASDYKDFYIC 213  
DB 267 VMQTGTSVSFGLFRRSPVAPAEKSGPVYKEPPGASVYVYRHCSLVPPEPSAHQYTVS 326  
QY 214 VNGSENKPIRSSYFTFQLONIYKPLPPVYLFTFRSSCEIKLWSIPLGPIPARCFDYE 273  
DB 327 V-----KHLQGGKFIHSYNHIQMEPPLNTLTKNRDS---YSLHMETQKMAVSFEIHTFQ 377  
QY 274 IEIHEDDTLVATVAVEN--ETTYLTKTNETROLCEVRSKVNICYSDGIMSEMSDQCV 331  
DB 378 VOYKKKSDSWEDSKTEMLDRAHSMDSLSQLEPDITSYCARVAVKPIISNYDGIWMSSEYTW 437

OY 332 EGEDLSKTLRLFWLPGFILLIVFYVTLGL 363  
: | | : | | : | | : | |  
Db 438 K-TDWMVMTL---WI---VLLIVFLITLTL 461

RESULT 14  
A29884  
prolactin receptor precursor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 28-Jul-2000  
C:Accession: A29884  
R:Butlin, J.M.; Jolicoeur, C.; Okamura, H.; Gagnon, J.; Ederly, M.; Shirota, M.; Banville  
Cell 53, 69-77, 1988  
A:Title: Cloning and expression of the rat prolactin receptor, a member of the growth hc  
A:Reference number: A29884; MUID:86165059; PMID:2832068  
A:Accession: A29884  
A:Molecule type: mRNA  
A:Residues: 1-310 <BOU>  
A:Cross-references: GB:M19304; NID:g206364; PIDN:AAA1937.1; PID:g206365  
C:Superfamily: cytokine receptor homology  
C:Keywords: transmembrane protein  
F:1/9/Domain: signal sequence #status predicted <SIG>  
F:20-310/Product: prolactin receptor #status predicted <MAT>  
F:31-216/Domain: cytokine receptor homology <CRS>

Query Match 7.8%; Score 165; DB 2; Length 310;  
Best Local Similarity 28.5%; Pred. No. 1.3e-05;  
Matches 63; Conservative 24; Mismatches 94; Indels 40; Gaps 10;

OY 131 SPQIGPETHVQDMDCVYNNQYLLCSMKPGIGVLLDTYNNLFYWEGLDHALQCVDTYKA 190  
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |  
Db 21 SPQKPEIH-----KCRSPDKETFTGWNPNPGTDGGLPTNYSILYSKEGKTYECPDY-KT 75

OY 191 DGQNGCRFPYLEASDYKDFYICVN-----GSSENKPIRSSYFTFQLONIYKPLPPVYLT 245  
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |  
Db 76 SGPN-SCFFSKQYTSIMKIIITIVNATNQMGSSSDPL-----YVDVYIYEPEPPRLT 129

OY 246 F-----TRESSEIKLWKSIP-LGPIPARCFDEIREDDTTLVTAIVENETYLTKTNE 300  
: | | | | | : | | | | | : | | | | | : | | | | | : | | | | |  
Db 130 LEVQOLKDKKTYLWYKSPPTITDVKTGFTMEYEIR-----LKPEAEWEIHFYGH 182

OY 301 TROL-----CFVRSKYNIVCSDDGIMSEWSKQWE 332  
: | | | | | : | | | | | : | | | | | : | | | | | : | | | | |  
Db 183 QTFKRVFDLYPGQKYLVTGRCK---PDHGYSRMSQESSVE 220

SUPT 15  
A41070  
prolactin receptor NB2 precursor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 12-Jun-1992 #sequence\_revision 12-Jun-1992 #text\_change 28-Jul-2000  
C:Accession: A41070; I55417  
R:Ali, S.; Pellegrini, I.; Kelly, P.A.  
J. Biol. Chem. 266, 20110-20117, 1991  
A:Title: A prolactin-dependent immune cell line (NB2) expresses a mutant form of prolact  
A:Reference number: A41070; MUID:92041834; PMID:1718958  
A:Accession: A41070  
A:Molecule type: mRNA  
A:Residues: 1-412 <ALI>  
A:Cross-references: GB:M74152; NID:g206389; PIDN:AAA41946.1; PID:g206390  
R:O'Neal, K.D.; Yu-Lee, L.Y.  
J. Biol. Chem. 269, 26076-26082, 1994  
A:Title: Differential signal transduction of the short, NB2, and long prolactin receptor  
A:Reference number: I55417; MUID:95014432; PMID:7929319  
A:Accession: I55417  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-412 <RSS>  
A:Cross-references: EMBL:U07567; NID:9641963; PIDN:AAA61784.1; PID:9641964  
A:Experimental source: NB2-11C cell line  
C:Superfamily: cytokine receptor homology  
C:Keywords: transmembrane protein

F:31-216/Domain: cytokine receptor homology <CRS>

Query Match 7.8%; Score 165; DB 2; Length 412;  
Best Local Similarity 28.5%; Pred. No. 1.8e-05;  
Matches 63; Conservative 24; Mismatches 94; Indels 40; Gaps 10;

OY 131 SPQIGPETHVQDMDCVYNNQYLLCSMKPGIGVLLDTYNNLFYWEGLDHALQCVDTYKA 190  
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |  
Db 21 SPQKPEIH-----KCRSPDKETFTGWNPNPGTDGGLPTNYSILYSKEGKTYECPDY-KT 75

OY 191 DGQNGCRFPYLEASDYKDFYICVN-----GSSENKPIRSSYFTFQLONIYKPLPPVYLT 245  
| | | | | : | | | | | : | | | | | : | | | | | : | | | | |  
Db 76 SGPN-SCFFSKQYTSIMKIIITIVNATNQMGSSSDPL-----YVDVYIYEPEPPRLT 129

OY 246 F-----TRESSEIKLWKSIP-LGPIPARCFDEIREDDTTLVTAIVENETYLTKTNE 300  
: | | | | | : | | | | | : | | | | | : | | | | | : | | | | |  
Db 130 LEVQOLKDKKTYLWYKSPPTITDVKTGFTMEYEIR-----LKPEAEWEIHFYGH 182

OY 301 TROL-----CFVRSKYNIVCSDDGIMSEWSKQWE 332  
: | | | | | : | | | | | : | | | | | : | | | | | : | | | | |  
Db 183 QTFKRVFDLYPGQKYLVTGRCK---PDHGYSRMSQESSVE 220

Search completed: January 24, 2003, 19:37:32  
Job time : 24 secs

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